44653, A 48452, A 48452, A 48451, A 48322, A 43272, A 533873, A 53855, A 31823, A 31823, A 31823, A 4268, A 44268, A

63253, 47653, 48452, 47652, 48451, 48451,

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence 52855, p. Sequence 53970, Sequence 51525, p. Sequence 51525, p. Sequence 31803, p. Sequence 18655, p. Sequence 18655,

Sequence 18655, Sequence 31888, Sequence 44265,

ALIGNMENTS

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US-11.056-3551-63253
US-11.056-3558-44653
US-11.056-3558-44652
US-11.056-3558-44651
US-11.056-3558-44651
US-11.056-3558-44651
US-11.056-3558-448450
US-10.449-902-52855
US-10.449-902-52855
US-10.449-902-52855
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                                                                                                                                                                                                                                                                                                         US-11-330-403-100-2
US-10-449-902-31888
US-10-449-902-44265
TYPE: PRT
ORGANISM: Homo sapiens
RESULT 2
US-10-449-902-30557
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                                                                                                                           6, 2006, 10:48:46 , Search time 75 Seconds
(without alignments)
138.397 Million cell updates/sec
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/ EMC_Celerra_SIDS3/prodata/1/pubpaa/USO6_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/prodata/1/pubpaa/USO3_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/prodata/1/pubpaa/USO8_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/prodata/1/pubpaa/USI3_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/prodata/1/pubpaa/USI3_NEW_PUB.pep:*
/ EMC_Celerra_SIDS3/prodata/1/pubpaa/USI3_NEW_PUB.pep:*
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                   GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-449-902-30557
US-10-449-902-33051
US-10-533-519-233
US-10-533-519-233
US-10-953-349-16530
US-10-953-349-16529
US-11-953-349-16529
US-11-056-358B-117326
US-11-056-358B-177326
US-11-056-358B-177326
US-11-056-358B-1777376
US-11-056-358B-177777
US-11-056-358B-17777
US-11-056-358B-17777
US-11-056-358B-17777
US-11-056-358B-17777
US-11-056-358B-17777
US-11-056-358B-17777
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.11-056-355B-117324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA New:*
                                                                                                                                                                                                                                                                                                                                358988 seqs, 90258633 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                          protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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APPLICANT: Chiang, Chih-Sheng
APPLICANT: Chiang, Chih-Sheng
APPLICANT: Simard, John J.L.
APPLICANT: Simard, John J.L.
APPLICANT: Simard, John J.L.
APPLICANT: Bac, Adrian Ion
APPLICANT: Liu, Xiping
TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
TITLE OF INVENTION: ANTIENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
FILE REFERENCE: MANNK.050CP1
CURRENT APPLICATION NUMBER: US/11/323,964
CURRENT APPLICATION NUMBER: US/11/323,964
PRIOR FILING DATE: 2005-12-29
PRIOR APPLICATION NUMBER: PI/155,288
PRIOR FILING DATE: 2005-06-17
PRIOR PAPLICATION NUMBER: 60/580,969
PRIOR PILING DATE: 2006-06-17
PRIOR APPLICATION NUMBER: 60/580,969
PRIOR APPLICATION NUMBER: 60/580,969
SRIOR DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PASTESQ for Windows Version 4.0
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publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 597; DB 7; Best Local Similarity 100.0%; Pred. No. 1.2e-55; Matches 115; Conservative 0; Mismatches 0;
US-11-329-964-11

; Sequence 11, Application US/11323964

; Publication No. US/20060159689A1

; GENERAL INFORMATION:
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Result Š.

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TYPE: PRT
ORGANISM: Homo sapien
FEATURE:
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US-10-449-902-43851
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
ITLE OF INVENTON: FULL-LENGTH PLANT CDNA AND USES THEREOF FILE REFERENCE: MOA-A0205Y1-US
CURRENT PELING DATE: 2003-62-29
PRIOR PILING DATE: 2003-62-29
PRIOR PLING DATE: 2002-05-30
PRIOR PLING DATE: 2002-02-31
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTHARE: Patentin Ver. 2.1
LENGTH: 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
19.9%; Score 119; DB 6; Length 232;
Best Local Similarity 20.7%; Pred. No. 7.9e-05;
Matches 34; Conservative 19; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 EVYCNGQLVFSKLSEQRFPSEFELRELIGNRLPDSQFGKNLEKV 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Oryza sativa
US-10-449-902-30557
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HAD APPLICANT: SCHORNEELD, JILL

SCHORNEELD, JILL

SCHORNEELD, JILL

SCHORNEELD, JILL

SCHORNEELD, JILL

SAPPLICANT: WILLIAMS, P. MICKEY

APPLICANT: WOOD, WILLIAM I.

TITLE OF INVENTION: RELATED DISEASES

TITLE OF INVENTION: COMPOSITIONS AND METHODSF OR THE TREATMENT OF IMMUNE

TITLE OF INVENTION: RELATED DISEASES

TITLE OF INVENTION: UNBER: LOS

CURRENT FILING DATE: 2005-04-28

FRIOR PILING DATE: 2003-10-30

PRIOR FILING DATE: 2003-10-30

PRIOR FILING DATE: 2003-10-30

SEQ ID NO 233

LENGTH: 87

TYPE.
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                                                                                                                                                                                                  Sequence 43851, Application US/10449902

Sequence 43851, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Poundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGIP FLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-A0205Y1-US

CURRENT FILING DATE: 2002-05530

PRIOR PILING DATE: 2003-05-39

PRIOR PILING DATE: 2002-05-30

PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 43851
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59 LGGTGAFEIEINGQLVFSKLENGGFPYEKDLIEAIRRASNGETLEKITNSRPP 111
                                   205 LQSSGAFEVYCNGDLVPSKLARQRFPSEFELRDLI-------NSRLP 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 LGGTGAFEIEINGQLVFSKLENGGPPYEKDLIEAIRRASNGETLEKITNSRPP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 LQSSGAFEVYCNGDLVFSKLAEQRFPSBFBLRDLI-------NSRLP 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-43851
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APPLICANT: ALEXANIROV, NICKOLAI et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SEQ ID NO 16529
LENGTH: 236
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                                                                                                                                                                                                                                                                                                                         95 PPEKPISNIATPGLGNTVYINFCSSCSYKGTAVTMKNMLEIALPGTEVILANYPPSLPKR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 LLSKLVPVVQIGVVGVVVAGEHIFPMLGFVAPPPWYYNLRANRFGTIASTWLLGNALQSF 214
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                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74; Gaps
ORGANISM: Glycine max
FEATURE:
NAME/KEY: misc feature
LOCATION: (228)...(228)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-16530
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// LOCATION: (229)

// OCTHER INFORMATION: Xaa can be any naturally occurring amino acid

US-10-953-349-16529
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                                                                                                                                                                                 Length 235;
                                                                                                                                                                                                                                       25; Indels
                                                                                                                                                                              Query Match
15.6%; Score 93; DB 6;
Best Local Similarity 19.1%; Pred. No. 0.045;
Matches 27; Conservative 15; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-953-349-16529; Sequence 16529, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 LQSSGAFEIYFNGXLVFSKLK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 LQSSGAFEIYFNGXLVFSKLK 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 LGGTGAFEIEINGOLVFSKLE 79
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                                                                                                                                                                                                                                                                                                                                                                                                ----- 95
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Sequence 16531, Application US/10953349

Publication to . US20060107345A1

GENERAL INFORMATION:
TITLE OF INVENTION: ENCONDED THERBY
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-15799US2

CURRENT FILE OF INVENTION WUMBER: US/10/953,349

CURRENT FILE OF DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3

SEQ ID NO 16531

LENGTH: 212
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Publication No. US20060107345A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REPRENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE PATENTIN Version 3.3
SEQ ID NO 16530
LENGTH: 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 LLSKLVPVVQIGVVGVVVAGEHIFPMLGFVAPPPWYYNLRANRFGTIASTWLLGNALQSF 191
                                                                                                                                                                                                                                             5 VRVV--YCGAXGYKSKYLQLKKKLEDEFPGRLDICGEGTPQATGFFEVNVAGKLIHSKKK 62
                                                                                                                                                                                                               23 VRIVVEYCEPCGFEATYLELASAVKEQYPG-IEI--ESRLGGTGAFEIEINGQLVFSKLE 79
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) LOCATION: (205)...(205)

OTHER INFORMATION: Xaa can be any naturally occurring amino acid

US-10-953-349-16531
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                                                                                                       Query Match
17.0%; Score 101.5; DB 6; Length 87;
Best Local Similarity 32.1%; Pred. No. 0.0017;
Matches 26; Conservative 21; Mismatches 25; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
15.6%; Score 93; DB 6; Length 212;
Best Local Similarity 19.1%; Pred. No. 0.039;
Matches 27; Conservative 15; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 PPEE----VEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEI
     ; LOCATION: 13
; OTHER INFORMATION: unknown amino acid
US-10-533-519-233
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US-10-953-349-16530
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Sequence 15768, Application US/10953349
Publication No. US20060107345A1
CENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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Publication No. US20060150283A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav

APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REPERENCE: 2750-15909US2

CURRENT FILING DATE: 2005-20-14

PRIOR APPLICATION NUMBER: 60/544,190

PRIOR PILING DATE: 2004-02-13

NUMBER OF SEQ ID NOS: 119966

SEQ ID NO 117326

LENGTH: 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.4%; Score 80; DB 7; Length 158; Best Local Similarity 30.0%; Pred. No. 0.64; Matches 24; Conservative 14; Mismatches 38; Indels
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Best Local Similarity 30.0%; Pred. No. 0.64;
Matches 24; Conservative 14; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           | PEATURE:
| NAME/KEY: peptide
| LOCATION: (1)..(158)
| TOTER INFORMATION: Ceres Seq. ID no. 13618700
| US-11-056-35SB-106087
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; OTHER INFORMATION: Ceres Seq. ID no. 13618700
US-11-056-355B-117326
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 106087
LENGTH: 158
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ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                            TYPE: prt
ORGANISM: Arabidopsis thaliana
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US-10-953-349-15768
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| Publication No. US2066107345A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYBEPTIDES
| TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYBEPTIDES
| TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYBEPTIDES
| TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYBEPTIDES
| TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYBEPTIDES
| TITLE OF INVENTION: 057799405
| CURRENT APPLICATION NUMBER: US/10/953,349
| CURRENT PELLING DATE: 2004-09-30
| SEQUENCE OF SEQUENCE OF
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Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
TITLE OF INVENTY SECRETED FROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 00766.000103.6
CURRENT APPLICATION NUMBER: US/11/395,249
CURRENT PILING DATE: 2006-04-03
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
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13.4%; Score 80; DB 7; Length 137;
Best Local Similarity 43.6%; Pred. No. 0.54;
Matches 17; Conservative 9; Mismatches 13; Indels
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13.4%; Score 80; DB 6; Length 158;
Best Local Similarity 30.0%; Pred. No. 0.64;
Matches 24; Conservative 14; Mismatches 38; Indels
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                                                                                                    Merberg, David
Treacy, Maurica
Agostino, Michael J.
Steininger II, Robert J.
Spaulding, Vikki
Wong, Gordon G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GTGAFEI-EINGOLVFSKLE 79
          Collins-Racie, Lisa A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Arabidopsis thalians
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: Homo sapiens
US-11-395-249-96
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U8-11-056-355B-106087
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US-10-953-349-10235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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APPLICANT:
APPLICANT:
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US-10-953-349-15767
US-10-953-349-15767
Sequence 15767, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROW, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŝ
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                                                                                                                                                                                                                                                                                                                                                                                   4 EPGQ--TSVAPPPEEVEP----GSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIES 57
                                                                                                                                                                                                                                                                                                                                                                                                                                  ----RING 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 EPGQ--TSVAPPPEEVEP----GSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIES 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 QPSQPATPVTPPPAEPKPQPVSTPSPKVSTKFSDVLAFSGPAPE-------RING 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OP INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR PILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 53080
LENGTH: 176
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                         22;
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13.4%; Score 80; DB 7; Length 176;
Best Local Similarity 28.3%; Pred. No. 0.74;
Matches 26; Conservative 12; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                          DB 6; Length 176;
                                                                                                                                                                                                                                                                                     13.4%; Score 80; DB 6; Length 176.
28.3%; Pred. No. 0.74;
tive 12; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  36 OPSOPATPVTPPPAEPKPOPVSTPSPKVSTKFSDVLAFSGPAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: peptide
LOCATION: (1)...(176)
COTHER INFORMATION: Ceres Seq. ID no. 13637661
US-11-056-355B-53080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 RL---GGTGAFEIEI-NGQLVFSKLENGGFPY 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 RL---GGTGAFEIEI-NGQLVFSKLENGGFPY 85
TITLE OF INVENTION: ENCONDED THERBY FILE REFERENCE: 2750-1579PUS2 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT FILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SOFTWARE: Patentin version 3.3 SEQ ID NO 15768 LENGTH: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 53080, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 28.3%
Matches 26; Conservative
                                                                                                                                                                                         ) TYPE: PRT

) ORGANISM: Glycine max

US-10-953-349-15768
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المراجعة الم

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:

December 6, 2006, 10:37:27; Search time 23 Seconds (without alignments) 481.084 Million cell updates/sec

US-09-824-787B-2 597 1 MSGEPGQTSVAPPPEEVEPG.......ASNGETLEKITNSRPPCVIL 115 Title: Perfect score: Sequence:

Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_80:* Database :

pirl:* pir2:* pir3:* 4 3 2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ì	Des	hypothetical prote			hypothetical prote	hypothetical prote	н	probable glutaredo	chalcone synthase	probable MRSA prot	hypothetical prote	CDA peptide synthe	hypothetical prote	phosphoribosylglyc	oxidoreductase Atu	probable oxidoredu	McrB-related prote	protein-export pro	two-component resp	2,3-bisphosphoglyc	alcohol dehydrogen	gamma-glutamyltran	[glutamate-ammonia	eph-related recept	large chain of NAD	hypothetical prote	probable histidino	adenosylmethionine	elongation factor	nrohahle tryntonha
	۵	T19747	T19755	AD2604	D97386	D83228	C82257	A72669	E86152	D72722	AD3542	T36249	T21526	E64485	AD2985	C98298	A75634	D87713	H83799	B64301	T18230	F70068	AI3417	148953	D97106	G83171	T03270	C69594	F86577	C72601
	DB	2	7	N	N	~	~	~	C3	~	~	0	0	П	~	0	N	N	0	~	~	~	~	(1	N	N	7	Н	7	~
	пg	255	258	101	101	96	97	243	395	469	101	3670	232	393	698	729	696	163	209	428	348	525	938	987	1507	347	413	448	282	467
*	tch tch	15.4	15.4	15.1	15.1	13.9	13.6	13.4	13.2	13.2	13.1	13.1	12.7	12.6	12.4	12.4	12.4	12.2	12.1	12.1	12.1	12.1	12.1	12.1	12.1	12.0	11.9	11.9	11.8	11.8
	Score	92	92	06	90	83	81	80	79	79	78.5	78	92	75.5	74	74	74	73	72.5	72.5	72	72	72	72	72	71.5	71	71	70.5	70.5
;			7	٣	4	S	9	7	80	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT 2

Argornerical protein C3SCS.3b - Caenorhabditis elegans
Dypothetical protein C3SCS.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19755
R;White, S.
R;White, S.
R;White, C.
A;Reference number: Z19173
A;Accession: T19755

chalcone isomerase	hypothetical prote	probable 3-hydroxy	outer membrane pro	protein F9C16.9 [i	hypothetical prote	involved in spore	molybdenum cofacto	phosphoribosylglyc	FMN oxidoreductase	proline dehydrogen	hypothetical prote	hypothetical prote	molybdopterin conv	methylated-DNA-[pr	hypothetical prote
T08006	C69433	T36703	S60142	D96503	G96828	H83788	E75151	D70632	F87472	153597	G89971	T12985	C69522	H72320	F84636
8	ď	~	~	~	~	7	~	N	7	7	7	~	~	~	~
241	489	504	673	946	167	411	159	419	430	1310	207	208	239	139	183
11.7	11.7	11.7	11.7	11.7	11.6	11.6	11.6	11.6	11.6	11.6	11.5	11.5	11.5	11.4	11.4
70	70	70	70	70	69.5	69.5	69	69	69	69	68.5	68.5	68.5	68	68
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

•	RESULT 1 T19747	
•	hypothetica C.Species: C.Date: 15- C.Accessior	hypothetical protein C35C5.3a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T19747
	submitted A;Referen A;Accessi	submitted to the EMBL Data Library, August 1996 A.Reference number: Z19173 A.Accession: T19747
25	A; Status: A; Molecul	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Wolecule Vype: DDR A:Readidnes: 1-255, cWIL.
	A; Experimen	A;Cross-references: UNIPARC:UP10000164317; EMBL:Z78417; PIDN:CAB01684.1; GSPDB:GN00028; (A;Experimental source: clone C35C5
:	A, Generates: A, Gene: CESP:C35C A, Map position: X A, Introns: 11/3;	A./Gene: CESP.C35C5.3a A;Map position: X A;Introns: 11/3; 34/1; 64/2; 100/2; 141/3
,	Query Ma Best Loc Matches	Query Match Best Local Similarity 18.0%; Pred. No. 0.2; Matches 24; Conservative 18; Mismatches 23; Indels 68; Gaps 2;
	ά	29 YCEPCGFEATYLELASAVKEQYPGIEIESR
	qq	
-	λõ	62TGAFEIEINGQLVFSKLEN 80
	qq	159 NPFERFGLGYPQILQHAHGNKMSSCMLVFMLGNLVEQSLISTGAFEVYLGNEQIWSKIES 218
	ò	81 GGFPYEKDLIEAI 93
	qq	219 GRVPSPQEFMQLI 231

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Query Match
15.4%; Score 92; DB 2;
Best Local Similarity 18.0%; Pred. No. 0.21;
Matches 24; Conservative 18; Mismatches

A;Gene: CESP:C35C5.3b A;Map poettion: X A;Introns: 11/3; 34/1; 67/2; 103/2; 144/3

C,Genetics:

29 YCEPCGFEATYLELASAVKEQYPGIEIESR----

| | ::::| GRVPSPQEFMQLI 234

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hypothetical protein PA3338 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Species: Psep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83228
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S., Joson, M.V.
Nature 406, 959-9544, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                selenoprotein W-related protein VC0982 [imported] - Vibrio cholerae (strain N16961 seroga
C,Species: Vibrio cholerae
C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: UNIPROT:Q9KTC1; UNIPARC:UPI00000C2E43; GB:AE004179; GB:AE003852; NID:
A,Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIFROT:O9HYQ7; UNIFARC:UPI00000C59C0; GB:AE004756; GB:AE004091; NID:
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: C92257
Stylesdelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

2, Rature 466, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A; Reference number: A82035; MUID: 20406833; PMID: 10952301
                                   A;Cross-references: UNIPROT:Q8UIR5; UNIPARC:UP100000D173B; GB:AE007869; PIDN:AAK86045.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   58
                                                                                                                                                                                                                                                                                                                                                                                                                           2 PTAKPEIVITYCTQCQWLLRAAWLAQELLSTFADDLGKVCLEPGTG--GVFRITCDGVQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 PGSGVRIVVEYCEPCGF--EATYL--ELASAVKEQYPGIEIESRLGGTGAFEIEINGQLV
                                                                                                                                                                                                                                                                                                                                                                            16 EVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPG-IEIESRLGGTGA-FEIEINGQL
                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                   Query Match
15.1%; Score 90; DB 2; Length 101;
Best Local Similarity 29.6%; Pred. No. 0.11;
Matches 24; Conservative 17; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 13.9%; Score 83; DB 2; Length 96; Best Local Similarity 31.2%; Pred. No. 0.49; Matches 25; Conservative 13; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 IWERKRDGGFPGPKELKQRIR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :::||| | ::|
WERKADGGFPEAKALKQRVR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 FSKLENGGFPYEKDLIEAIR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 VFSKLENGGFPYEKDLIEAIR
                                                                  C,Genetics:
A,Gene: AGR_C_387
A,Map position: circular chromosome
A; Residues: 1-101 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Accession: D83228
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-96 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: C82257
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: PA3338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein Atu0228 [imported] - Agrobacterium tumefaciens (strain CS C)Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: lu-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AD3604
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
by 3386
hypothetical protein AGR_C_387 [imported] - Agrobacterium tumefaciens (strain C58, Cerec hypothetical protein AGR_C_387 [imported] - Agrobacterium tumefaciens (strain C58, Cerec C; Species: Agrobacterium tumefaciens
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C; Date: 30-Sep-30386
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Soctt, C.; Lappas, C.; Markelz, B.; Science 294, 233-2332, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUD:21608551; PMID:11743194
A; Genus: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: UNIPROT:Q8UIRS; UNIPARC:UP100000173B; GB:AE008688; PIDN:AAL41250.1; Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Accession: AD2604
                                                                                                                                                                                                                                                                                                                                                                                            162 NPFERFGLGYPQILQHAHGNKMSSCMLVFMLGNLVBQSLISTGAFEVYLGNEQIWSKIES 221
                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --TGAFEIEINGQLVFSKLEN 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 EVEPGSGVRIVVEYCEPCGPEATYLELASAVKEQYPG-IEIESRLGGTGA-FEIEINGQL 73
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                                                                                                                                                                                                                                                                  68;
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                                                                                                                                                                                            DB 2; Length 258;
                                                                                                                                                                                                                                                              23; Indels
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17; Mismatches

24; Conservative

Query Match Best Local Similarity

Best Loca Matches

ò 8 ò 쉱

A)Cross-references: UNIPROT:Q8UIR5;
A)Experimental source: strain C58 (I C)Genetics: A)Gene: Atu0228
A;Map position: circular chromosome

A,Status: preliminary A,Molecule type: DNA A,Residues: 1-101 <KUR>

74 VFSKLENGGFPYEKDLIEAIR 94

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C,Accession: D72722
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahtawa, H.; Takahtya, M.; Msauda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K. DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyn A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-469 <KAW>
A,Cross-references: UNIPROT:Q9YFC4; UNIPARC:UPI000005DAC5; DDBJ:AP000059; NID:g5103911; I
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R,DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltsman, B.; Selvkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 A,71tle: The genome sequence of the facultative intracellular pathogen Brucella melitens) A,Reference number: AD3252; PMID:11756688
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A;Experimental source: strain 16M
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                                                                                                                                                                                            328 -----GGIAAFE-----ENGGYMHPPHQYVRDGGMKAALLLAMLRAT-GESLS 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 IESRLGGTGAFEIEINGQLVFSKLENGGF-----PYEKD-----LIEAIRRASNGETLE 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Species: Aeropyrum pernix
C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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                                                                                           50; Gaps
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                          Length 395;
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                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
                          Query Match 13.2%; Score 79; DB 2; Lei
Best Local Similarity 24.1%; Pred. No. 6;
Matches 32; Conservative 15; Mismatches 36;
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Local Similarity 27.6%; Pred. No. 7.3;
es 35; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: phosphomannomutase
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327 KLEKEKLESSRRA 339
                                                                                                                                                                                                                                                                                                                                                                                                                    84 PYEKDLIEAIRRA
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A;Residues: 1-101 <KUR>
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                       09
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Matches
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C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: O-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: A72669
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Takah DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: A72669
A;Status: per A72669
A;Status: Pe
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                                                                                                                                                                                      24 RIVVEYCEPCGF--EATYL--ELASAVKEQYPGIEIESRLGGTGAFEIEINGQLVFSKLE
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                                                            13.6%; Score 81; DB 2; Length 97; 29.3%; Pred. No. 0.78;
                                                                                                                         33; Indels
                                                                                                                            14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 1
C;Superfamily: type III polyketide synthase
                                                                                                                                                                                                                                                                                                                      80 NGGFPYEKDLIEAIR 94
                                                                                                                                                                                                                                                                                                                                                                                  63 EĞĞFPEAKVLKQRVR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain K1
                                                         Query Match
Best Local Similarity 29.33
Matches 22; Conservative
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Best Local Similarity
Matches 22; Conserv
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A;Residues: 1-395 <STO>
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A; Map position:
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12.7%; Score 76; DB 2; Length 232; 15.1%; Pred. No. 6.4; ive 19; Mismatches 31; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 FSKLENGGFPYEKDLIEAI 93
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Start codon: TTG
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Matches 31; Conservative
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                            Best Local Similarity
Matches 21; Conserv
                                        A; Map position: 5
A; Introns: 23/1; 134/3
    A; Gene: CESP: F28H7.4
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                                                                                                                                                            Query Match
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R;Saunder, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.B. A;Baunder, D.C.; Harris, D.; March 1999
A;Reference number: Z21602
A;Accession: T36249
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Style perfect of the control o
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A.Accession: T21526
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-232 <WIL>
A.Gross-references: UNIPROT:Q19892; UNIPARC:UPI0000135A34; EMBL:Z72508; PIDN:CAA96637.1;
A.Rexperimental source: clone F28H7
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: DNA
A,Residues: 1-3670 <SAU>
A,Crose-references: UNIPROT:Q9Z4XE; UNIPARC:UPI0000DAFIE; EMBL:AL035640; PIDN:CAB38517
A,Experimental source: strain A3(2)
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                                                                                                                                                                                                                                                                                                             24 RIVVEYCEPCGFEATYLELASAVKEQYPG--IEIESRLGGTGAFEIEI-----NGQLVFS 76
                                                                                                                                                                                                                                                                                                                                                                             6 RISITYCTQCNWLLRAAWMAQELLQTFGQDLAEVALRPGTGGVFEIRVQMPDGSEELIWE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 YLELASAVKEQYPGIEIESRLGGTGAFEIEINGQLVFSKLENGGFPYEKDLIEAIRRASN 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypochetical protein F28H7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Dates: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21526
R;Barks, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDA peptide synthetase II SCE63.02c [imported] - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Decies: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 12-Jul-2004 C;Accession: T36249 Rsquence_revision 03-Dec-1999 #text_change 12-Jul-2004 R;Saunder, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Ra:
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                                                                                                                                                                                                                                        7,
                                                                                                                                                        13.1%; Score 78.5; DB 2; Length 101; 26.9%; Pred. No. 1.4;
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Pred. No. 97;
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                                                                                                                                                                                                                                34;
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                                                                                                                                                                                                                                    16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 KLENGGFPYEKDLIEAIR 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 RKRDGGFPEAKVLKQRVR 83
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1 Similarity 31.7%;
26; Conservative 1.
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Best Local Similarity
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Matches 21; Conserv
C,Genetics:
A,Gene: BMEII0262
A,Map position: II
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phosphoribosylglycinamide formyltransferase 2 (EC 2.1.2.-) MJ1486 [similarity] - Methanoc Cispecies: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: 10.5ep-1999 #sequence_revision 10.5ep-1999 #text_change 09-Jul-2004
C;Accession: E64486
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, C; Relch, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Fson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Bordovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; Altile: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii. A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: E64485
A;Accession: E64486
A;Molecule type: DMID: Accession of shown, translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Residues: 1:393 <BUL>
A,Cross-references: UNIPROT:Q58881; UNIPARC:UPI0000132B6F; GB:U67589; GB:L77117; NID:g28;
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A;Note: cofactor magnesium
C;Superfamily: phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain; pl
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;29-371/Domain: phosphoribosylaminoimidazole carboxylase carbon dioxide-fixation chain l
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                                                                                      86 INLTIVFSVSČGYKQAFNQFYEFAKEKÝPGLVÍEGGNFSPDFWKGCLAQIVGVAKIGLIA 145
                                                                                                                                                                                                                                                                       146 IVITGSNPFEYIGFGYPQILQTAHYNRFSYSLLVFMIGNLFESTLSSTGAFEIFLGDKQI 205
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23 VRIVVEYCEPCGFEATYLELASAVKEQYPGIEI----
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ster, E.W.

A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Reference number: AB2577; MUID:21608550; PMID:11743193
A,Rocession: AD2985
A,Ratus: preliminary
A,Molecule type: DNA
A,Residues: 1-698 «KUR>
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: C98298
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Status: preliminary
A/Molecule type: DNA
A/Residues: 1-729 «KUR»
A/Cros6-references: UNIPROT:Q8UA89; UNIPARC:UP100000D2209; GB:AE007870; PIDN:AAK89909.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 CTFNLNPRAASIDTPLHGFVPFDHVDH----MHPDAIIAIAASKNSKEL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 -----TGAFEIEINGQLVFSKLENGGFPYEKDLIEAIRRASNGETL 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 12.4%; Score 74; DB 2; Length 698
Best Local Similarity 22.9%; Pred. No. 35;
Matches 25; Conservative 20; Mismatches 38; Indels
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A;Gene: AGR L_2690
A;Map position: linear chromosome
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

December 6, 2006, 10:26:47; Search time 148 Seconds (without alignments) 718.762 Million cell updates/sec Run on:

US-09-824-787B-2 597 1 MSGEPGQTSVAPPPEEVEPG......ASNGETLEKITNSRPPCVIL 115 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

2849598 Total number of hits satisfying chosen parameters: 2849598 segs, 925015592 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Re

Description	Q9brt3 homo sapien	Q9cq86 m adult mal	Q5zih7 gallus gall		Q802f5 brachydanio	Q802g8 brachydanio					Q7qf18 anopheles g	_			P63302 homo sapien	_	Q95kl4 sus scrofa	Q802g9 brachydanio			-			P63300 mus musculu	P63301 rattus norv		5 arabi	c,	٠.	3 vibrio	Q7mms1 vibrio vuln
ΠD	Q9BRT3 HUMAN	Q9CQ86_MOUSE	Q5ZIH7 CHICK	Q3ZLC7_OREMO	Q802F5_BRARE	Q802G8_BRARE	Q4T504 TETNG		Q8H6T4_CHLRE	Q4JBM6_SULAC	Q7QFL8 ANOGA	Q8S227 ORYSA	Q3QTH4 9RHOB	HSP6_HETGL	SEPW1 HUMAN	SEPW1_MACMU	SEPW1 PIG	Q802G9 BRARE	Q5NVB2_PONPY	Q568W0_BRARE	SELT ARATH	SELV HUMAN		SEPW1 MOUSE	SEPW1_RAT	Q61517 ORYSA	Q8W1E5 ARATH	Q3XA62_METFL	Q2KDL9 RHIET		Q7MMS1_VIBVY
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Score	597	537	435.5	288	273	221.5	218	148.5	137.5	137	132.5	119	116.5	114.5	112.5	ä	112.5	112.5	112.5		110.5	110.5	109	107.5	107.5	104	103.5	101	100	66	66
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SEPW1 SHEEP Q36PV6 MARHY Q3WXN7 PRHIZ Q87RH7 VIBPA	Q60CA7_METCA Q92SU7_RHIME Q7PVR5_ANOGA	Q802F2_BRARE Q7QZL6_GIALA SELT1_CAEEL	QSYEVI_CHLS6 QBUIRS_AGRTS QSU4CO_MOUSE
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STRAIN-CSTBL/61, TISSUE=Aorta and vein, Brain, Pancreas, and Tongue;
X PubMed=16141072; DOI=10.1126/science.1112014;
A Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
A Cyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
A Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
A Davis M.J., Wilming L.G., Aldinis V., Allen J.R.,
A Ambesi-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L.,
A manbesi-Impiombato A., Apweller R., Aturaliya R.N., Bailey T.L.,
A manbesi-Impiombato A., Apweller R., Aturaliya R.N., Balley T.L.,
A dambesi-Impiombato V., Christoffels A., Clutterbuck D.R.,
Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
A di Bernardo D., Down T., Engercom P., Fagiolini M., Faulkner G.,
R Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
Georgii-Hemming P., Gingeras T.R., Gojobori T., Garen R.E.,
A Gustincich S., Harbers M., Haysahi Y., Hensch T.K., Hirokawa N.,
A Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
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                                                                                                                                                                                                                                                                                                   1 MSGEPGQTSVAPPPEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLG
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Aorta and vein, Brain, Pancreas, and Tongue; MEDLINE=9927953; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001, sequence version 1.
07-FEB-2006, entry version 24.
Adult male tongue CDNA, RIKEN full-length enriched library,
clone: 2310051814 product: hypothetical protein, full insert sequence
(Adult male brain cDNA, RIKEN full-length enriched library,
clone: 071001H16 product: hypothetical protein, full insert sequence)
(10 day old male pancress CDNA, RIKEN full-length enriched library,
clone: 1810046519 product: hypothetical protein, full insert sequence)
(Adult male aorta and vein CDNA, RIKEN full-length enriched library,
clone: A530099524 product: hypothetical protein, full insert sequence)
(RIKEN CDNA, 1810046519).
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                   Length 115;
                                                                                                                                                                                                                                 100.0%; Score 597; DB 2; Length 1 100.0%; Pred. No. 8e-51; ive 0; Mismatches 0; Indels
                                                                                                              LinkHub; Q9BRT3; -.
GO; GO:0008430; F:selenium binding; IEA.
GO; GO:0045454; P:cell redox homeostasis; IEA.
InterPro; IPR011893; CXXU_selWTH; 1.
TIGRRPAMS; ITGR02174; CXXU_selWTH; 1.
SEQUENCE 115 AA; 12403 WW; 5D8B911C0F23DDC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QGCQ86_MOUSE PRELIMINARY; PRT; 115 AA.
Q9CQ86;
                          EMBL; BC006006; AAH06006.1; -; mRNA.
EMBL; A7490253; AAOB5461.1; -; mRNA.
EMBL; AYS08814; AAR92035.1; -; mRNA.
Ensembl; ENSG00000141741; Homo sapiens.
HGNC; HGNC; 28230; C17orf37.
                                                                                                                                                                                                                                                 Best Local Similarity 100.0
Matches 115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=1810046J19Rik;
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                                                                                                                                                                                                                                                                                                                                                                       61
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RECEDING SEQUENCE.

REALINE-CSTBL/64; TISSUE-Aorta and vein, Brain, Pancreas, and Tongue; RX MEDLINE-CSTBL/64; TISSUE-Aorta and vein, Brain, Pancreas, and Tongue; RX OKZAZKI Y. FUTUND M., RABUKAWA T., Adachi J., Bono H., Kondoo S., RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Mikaido II., Osato N., Bult C., Hume D.A., Quackenbush J., Radalare, Dragani T.A., Patcher C., Hume D.A., Quackenbush J., Rabala E., Dragani T.A., Patcher C., F., Forrest R.W., Frazer K.S., RA Dalla E., Dragani T.A., Pitcher C.F., Forrest R., Gough J., RA Garasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., RA Gariboldi M., Gissi C., Godzik A., Gough J., Axwaji H., Kawasawa Y., Kedzierski RM., King B.L., RA Konadaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Mancaka M., Marchionni L., McKenzie L., Miki H., RA Petrochkin I.V., Lee Y., Lenhard B., Lyons P.A., Radashim T., Numaca K., Okido T., Pavan W.J., Pertea G., Pesole G., Radgashima T., Numaca K., Okido T., Pavan W.J., Pertea G., Pesole G., RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Sandelin A., Schneider C., Sample C.A., Garanic M., Sanda K., Ashalawa T., Pulkuda S., Manining L.G., Wynbhaw-Boris A., Yanagisawa M., Yang I., Yang I., Yang I., Ray Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shinasaki A., Yashiishio M., Yashiishi Y., Ishii Y., Lich M., Kagawa I., Rayanishia A., Yashiino M., Zhiaya K., Ishiaya A., Hashizume W., Imotani K., Ishii Y., Lich M., Kagawa I., Ryanishia M., Yanguishia M., Yani Z., Rayanishia M., Yashiino M., Lichi Y., Lichi Y., Lichi Yanguishia M., Yashiino M., Lichi Y., Lichi Yanguishia M., Yashiino M., Lichi Y., Lichi Yanguishia M., Yanguishia M., Yashiino M., Lichi M., Kagawa I., Rayanishia M., Yashiino M., Lichi M., Kagawa I., Lander E.S., Rogers J., Lander E.S., Rogers J.,
RA Jakt M., Kanapin A., Katch M., Kawasawa Y., Kelso J., Kitamura H., RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K., Ra Kutcockhin I.V., Lareau L.B., Lazarevic D., Lipovich L., Liu J., RA Liuni S., Madul Babu M., Madera M., Marchionni L., RA Motsagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Mg P., RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Chara O., Ra Recrowsky N., Plazza S., Reed J., Reed J., Feld J.F., Ring B.Z., Ringwald M., RA Rost B., Run Y., Salzberg S.L., Sandellin A., Schneider C., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Takenaka Y., Takinawa H., Shimada K., Silva D., Sinclair B., Takenaka Y., RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ra Vamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Ratanond S.M., Teaadale R.D., Liu E.T., Brusic V., Quackenbush J., Rawashima T., Kojima M., Kato T., Kawaji H., Kawagashira N., Rawashima T., Kojima M., Kato T., Kawaji H., Kawashins J., Nahio T., Nahio T., Suzuki S., Ra Hadanishi M., Waki K., Watanishi Y., Suzuki H., Kawashi T., Rawashi J., Marashi T., Suzuki S., Ra Hadashizari Y., Suzuki T., Suzuki H., Kawashi J., Rawashi J., Marashi J., Suzuki S., Ra Hadashizari Y., Suzuki Y., Suzuki Y., Suzuki Y., Ra Hadashizari Y., Suzuki Y., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Aorta and vein, Brain, Pancreas, and Tongue; PubMed=16141073; DOI=10.1126/science.1112009; RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; Manisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Aorta and vein, Brain, Pancreas, and Tongue, MEDILINE=2108566; PubMed=11217851, DO=10.10138/35055500; Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The transcriptional landscape of the mammalian genome.";
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Nature 420:563-573(2002).
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A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gasererland T., Gissi C., King B., Kochiwa H., Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Puruno M., Ano H., Baldarelli R., Barsh G., Blake J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamcto N., Saski H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitteker C., Wilming L., Hassegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CS7BL/6J; TISSUE=Brain, Pancreas, and Tongue;
A Arakawa T., Azawa K., Akahira S., Akimura T., Arai A., Aono H.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramcto K., Hiracka T., Hori F.,
A Hanagaki T., Hara A., Hayatsu N., Hiramcto K., Hiracka T., Hori F.,
A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Sano H., Saaki D., Shibata K., Shibata Y., Sakinagawa A., Sakiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Supmitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Pukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hanagaki T., Hizamce M., Hashizume W., Hayatsu N., Hiramcto K., Hiracka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Mateuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohao M., Ohasto N., Okazaki Y., Salto R., Saltoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibate K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Towaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/63; TISSUE=Aorta and vein, Brain, Pancreas, and Tongue; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramateu M., Hayashizaki Y., Shibata K., Itoh M., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., TICOM M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishire T., Harada A., Yamamoto R., Matsumura S., Hazama M., Nishire T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Isawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Riki integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                              1 MSGEPGQTSVAPPPEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLG
                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SGEPGQTSVAPPPEEVEPGSG-------VRIVVEYCEPCGFEATYLELASAVKEQ
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         MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J., Fledler P., Kutter S., Blagodatski A., Kostovaka D., Koter M., Plachy J., Carninci P., Hayabhizaki Y., Buerstedde J.M., "Full-length cDNAs from chicken bursal lymphocytes to facilitate
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                                                                                                                                                                                    89.9%; Score 537; DB 2; Length 115;
89.6%; Pred. No. 6.7e-45;
iive 4; Mismatches 8; Indels
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SEQUENCE 126 AA; 13438 MW; 12B8498FD40DBB6D CRC64;
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GO; GO:0008430; F:selenium binding; IEA.
GO; GO:004544; P:cell redox homeostasis; IEA.
TIGRPRO; IPR011893; CXXU selWTH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 AA
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QSZIH7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-NOV-2004, sequence version 1. 07-FEB-2006, entry version 7. Hypothetical protein. ORFNames-RCJMB04 26b22, Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Biol. 6:R6-R6(2005)
                                                                                                                                                                                                                           Matches 103; Conservative
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STRAIN=CB; TISSUE=Bursa;
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QSZIH7_CHICK
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MEDLINE=22796661; PubMed=12915322; DOI=10.1016/S1567-133X(03)00054-1;
Thisse C., Degrave A., Kryukov G.V., Gladyshev V.N.,
Obrecht-Pflumio S., Kryukov G.V., Thisse B., Lescure A.;
"Spatial and temporal expression patterns of selenoprotein genes
during embryogenesis in zebrafish.";
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.7%; Score 273; DB 2; Length 95
54.3%; Pred. No. 6.2e-19;
ive 16; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       95 AA; 10572 MW; 05A25E769DDFDD0B CRC64;
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                                                                                                                                 EMBL, AY221261, AAO65270.1; -; mRNA.
Ensembl, ENSDARG0000038228; Danio rerio.
ZFIN; ZDB-GENE-030428-1; sepw2a.
GO; GO:0008430; F:selenium binding; IEA.
InterPro; IPR011893; CXXU selWTH.
TIGRFAMS; TIGR02174; CXXU selWTH; 1.
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Ensembl; ENSDARG0000038227; Danio rerio.
ZFIN; ZDB-GRNE-030428-2; sepw2b.
GO; GO:0008430; F:selenium binding; IEA.
InterPro; IPR011893; CXXU selWTH.
TIGRFAMS; TIGR02174; CXXU selWTH; 1.
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Expr. Patterns 3:525-532(2003).
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Best Local Similarity 54...
Best Local Similarity 54...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Profile analysis of expressed sequence tags derived from the ovary of tilapia, Oreochromis mossambicus.";
Aquaculture 251:537-548(2006).
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NUCLEOTIDE SEQUENCE.

NUCLEOTIDE SEQUENCE.

NEDLING=22796661; PUBMed=12915322; DOI=10.1016/S1567-133X(03)00054-1;

Thisse C., Degrave A., Kryukov G.V., Gladyshev V.N.,

Obrecht-Pflumio S., Krol A., Thisse B., Lescure A.;

"Spatial and temporal expression patterns of selenoprotein genes
during embryogenesis in zebrafish.";
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygli, Neopterygli, Taleosteli, Suceleleostel, Neoteleostel,
Acanthomorpha, Acanthopterygli, Percomorpha, Perciformes, Labroidei,
Cichlidae, African cichlids, Pseudocrenilabrinae, Tilapiini,
                                                                                                                                                                                                                                                                                                                                  Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-SEP-2005, integrated into UniProtKB/TrEMBL.
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OT-FBB-2006, entry version 9.
Selenoprotein W2a.
Name-sepw2a;
                                                                                                                                                                                                                                      27-SEP-2005, sequence version 1. 07-MAR-2006, entry version 4. Selenoprotein W2a.
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Q802F5;
                                                                                                                                                 PRELIMINARY;
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   121 PPCTIL 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8127;
                                                                                                                              Q3ZLC7;
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Matches

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PRT;
                                                                                                            ORFNames=CG15456, Dmel_CG15456;
                                                                              07-FEB-2006, entry version 26
               PRELIMINARY;
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                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                             NCBI_TaxID=7227;
           Q9VRAO DROME
Q9VRAO;
29VRA0 DROME
                NUCLECTIDE SEQUENCE.

PUDMed=15496914; DOI=10.1038/nature03025;

A Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,

Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,

Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,

Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,

Anthouard V., Jubin C., Cattolico L., Poulain J., De Berardinis V.,

Riemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

Relis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,

Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

Laudet V., Schachter V., Weiseschbach J., Roset Crollius H.;

"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 GFEATYLELASAVKEQYPGIEIESRLGGTGAFEIEINGQLVFSKLENGGFPYEKDLIEAI
                                                                                                                                                                         19-JUL-2005, sequence version 1.
19-JUL-2006, entry version 4.
Chromosome undetermined SCAF9556, whole genome shotgun sequence (Chromosome undetermined SCAF9556, whole genome shotgun sequence). ORNames=GSTENG00007059001, GSTENG00007180001;
Tetracdon nigroviridis (Green puffer).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontidae; Tetradontidae; Tetradontiformes; Tetradontoidea; Tetradontidae; Tetradonn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope, Whitehead Institute Centre for Genome Research,
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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51.2%; Pred. No. 1.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; CAAE01009476; CAF92028.1; -; Genomic_DNA.
EMBL; CAAE01009556; CAF92112.1; -; Genomic_DNA.
                  83 FPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 115
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GO; GO:004545; P:cell redox homeostasis; IEA.
TIGRPAMS; TIGR02174; CXXU_selWTH; 1.
                                 integrated into UniProtKB/TrEMBL
                                                                                                                               89 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vertebrate proto-karyotype.";
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                                                                                                                               PRELIMINARY;
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Q4T504;
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Matches

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RESULT

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REAL MEDILINE-20196006, PubMed=10731132; DOI=10.1126/science.287.5461.2185, Adams M.D. Celniker S.E., Holf R.A., Grans C.A., Gocapus J.D., RA Amanatides P.G., Scherer S.E., Lip P.W., Hoskins R.A., Galle R.F., Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandrell M.D., Zhang O., Chen L.X., Radon R.C., Rogers Y.-H.C., Blazel R.G., Clampe M., Pfeiffer B.D., Randon R.C., Rogers Y.-H.C., Blazel R.G., Mellon C.R., Miklos G.L.G., Abril J.F., Agbayari A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bassley E.M., Bench M.R., Benco P.V., Bernam B.P., Bandari D., Bolshakov S., Borkova D., Borcham M.R., Bouck J., Brokstein P., Bernah M.R., Bouck J., Bullke C., Davenport L.B., Davies P., R. Borkova D., Borcham M.R., Bullke C., Davenport L.B., Davies P., R. Durbin R.J., Evalgelista C.C., Ferraz C., Ferriera S., Pleischmann W., R.A. Benco R., Godriellan A.E., Gabra M., Didaser K., Godriellan A.E., Gabra M., Davies P., R. Houskow D., Borther M., Gabriellan A.E., Gabra M., Mei M.H., Ibegwam C., Adali M., Kalush F., Kalush F., Karavitz S., Kulp D., Lai Z., Liang Y., Liu X., Mattei B.E., Kodira C.D., Kraft C., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Liu X., Mattei B.E., McIntosh T.C., Morris J., Mornheria A., Mount S.M., Moyn W., Murphy B., Murphy L., Murzhy D.M., Nelson D.L., Raines D.M., Nithanna N.V., Morbary C., Morris J., Morbarson D.L., Raines D.M., Pittuan G.S., Pan S., Pollsker D., Wang A.H., Wang A.H., Wang S., Yao Q.A., Shen H., Spradling A.C., Stapleton M., Strong R., Sun E., Syradling R.C., Zhan M., Strong R., Sun E., Syradling R.C., Zhan M., Strong R., Sun E., Syradling R.C., Zhan M., Strong R., Zhong S., Yao Q.A., R., Benner S., Spradling A.C., Stapleton M., Stung G., Zhong W., Zhon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22456065; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a Whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
01-MAY-2000, integrated into UniProtKB/TrEMBL
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                                                     01-MAY-2000, sequence version 1.
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Query Match
Best Local Similarity
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SEQUENCE
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SULAC
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Q4JBM6
     요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                          MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                             Berkeley Drosophila Genome Project;
Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
Yu C., Rubin G.,
                                                                                                                                                                                                                                                                 Lewis S.E., "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-2006) to the EMBL/GenBank/DDBJ databases.
--- INTERACTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Drosophila melanogaster release 4 sequence.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LinkHub; Q9VRAO; --
GO; G005515; P: Procein binding; IPI.
InterPro; IPRO11893; CXXU_eelWTH.
InterPro; IPRO11941; Perredoxin.
InterPro; IPRO1174; CXXU_eelWTH: 1.
SEQUENCE 95 AA; 10506 WW; A4564893BF263FD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Selenoprotein SelWi.
Chlamydomonas reinhardtii.
Eukaryote, Virtdiplantes; Chlorophyta; Chlorophycese;
Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                 systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
  a genomics perspective.";
Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 PPYEKDLIEAIRRASNGETLEKITNSR-PPCVIL 115
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NUCLEOTIDE SEQUENCE.
                                                                        NUCLEOTIDE SEQUENCE
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QBH6T4;
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084674 CH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 SGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLGGTGAFEIEINGQLVFSKLEN 80
Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRANT=ATCC 33909 / NUTB 11770 / DSM 639;
PubMed=15995215; DOI=10.1128/JB 187.14.4992-4999.2005;
Chen L., Bruegger K., Skovgaard M., Redder P., She Q., Torarinsson E.,
Greve B., Awayez M., Zibat A., Klenk H.-P., Garrett R.A.;
"The genome of Sulfolobus acidocaldarius, a model organism of the
Crenarchaeocia.";
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                        32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; CP000077; AAY79803.1; -; Genomic_DNA.
GO; GO:0008430; F:selanium binding; IEA.
GO; GO:0045454; P:cell redox homeostasis; IEA.
InterPro; IPR011893; CXXU selWTH.
TIGRRAMS; TIGR02174; CXXU selWTH.
Complete proteome; Hypothetical protein.
SEQUENCE 80 AA; 9219 MW; 607FF3E75889F304 CRC64;
                                                                                                                                                                                                                                                                                                   88 AA; 9690 MW; DF27CBB4780E1128 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
22.9%; Score 137; DB 2;
Best Local Similarity 31.2%; Pred. No. 1.3e-05;
Matches 25; Conservative 21; Mismatches 32.
                                                                                                                                                                                                                                                                                                                                                          23.0%; Score 137.5; DB 2 37.2%; Pred. No. 1.3e-05;
                                                                             EMBL, AF494050; AAN32901.1; -; mRNA.
GO; GO:0008430; F:selenium binding; IEA.
GO; GO:004544; P:cell redox homeostasis; IEA.
TIGREPARS; TIGR02174; CXXU_selWTH; 1.
Selenium; Selenocysteine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 ENGGFPYEKDLIEAIRRASNGETLEK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KRFPDSQEILKELSKKATAQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-AUG-2005, sequence version 1.
07-FEB-2006, entry version 3.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OrderedLocusNames=Saci 0387;
Sulfolobus acidocaldarius.
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Q4JBM6;
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Q3QTH4_9RF
          SO WE DO NOT SO SO SERVING SERVING SO SERVING SO SERVING 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 CGFEATYLELASAVKEQYPGIEIESRLGGTGAFEIEINGQLVFSKLENGGFPYEKDLIEA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                            15-DEC-2003, integrated into UniProtKB/TrEMBL.
07-DEC-2004, sequence version 2.
07-EEB-2006, entry version 8.
ENSANGPO0000007373 (Fragment).
ORFNames=ENSANGG0000005563;
Anopheles gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anophelinae; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nāme=P0446G04.43-2; Synonyms=P0460C04.2-2;
Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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07-FEB-2006, entry version 13.
Hypothetical protein P0446G04.43-2 (Hypothetical protein P0460C04.2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Anopheles gambiae Sequence Committee;
Submitted (ARR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 AA; 10351 MW; DC3808C7B37D16C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AAAB01008846; EAA06627.2; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0008430; F:selenium binding; IEA. CO:0008430; P:selenium binding; IEA. CO: GO:0045454; P:cell redox homeostasis; IEA. IEA. ITGREPEO; IPRO11893; CXXU_selWTH; 1.
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                                                                        93 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Anopheles gambiae Sequence Committee; "Anopheles gambiae re-annotation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 IRRASNGETLEKITNSR-PPCVI 114
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                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                 PRELIMINARY;
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Q8S227;
                                                              ANOGA
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RESULT 11
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127 PFLQVGAMATLMAGDQIFPRFGMVPPPWYYSLRANRFGTMATIWLFGNFAQSFLQSSGAF 186
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                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Larimer F., Land M.; "Annotation of the draft genome assembly of Silicibacter sp. TM1040.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 PEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEI---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----ESRLGGTGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
Hammon N., Israni S., Pitluck S., Richardson P.;
"Sequencing of the draft genome and assembly of Silicibacter sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Silicibacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 232;
                                                                                                                                                                                                                                                                         "The genome sequence and structure of rice chromosome 1."; Nature 420:312-316 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 EIEINGQLVFSKLENGGFPYEKDLIEAIRR----ASNGETLEKI 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 EVYCNGQLVFSKLSEQRFPSEFELRELIGNRLPDSQFGKNLEKV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.9%; Score 119; DB 2; Length 23 20.7%; Pred. No. 0.0027; ive 19; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25385 MW; 7011E960E7909E4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 AA
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP003252; BAB89601.1; -; Genomic_DNA.
EMBL; AP004366; BAB92910.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q3QTH4 9RHOB PRELIMINARY; PRT; Q3QTH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2005, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-2006, entry version 3. Selenoprotein W-related.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Silicibacter sp. TM1040.
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232 AA; 25
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Best Local Similarity
Matches 34; Conserv
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Name=SEPW1; Synonyms=SELW;
                                     39; Conservative
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          Query Match
Best Local Similarity
Matches 39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                 Selenoprotein W.
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                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLECTIDE SEQUENCE [MRNA].
MEDLINE=21204659; PubMed=11310741;
MEDLINE=21204659; PubMed=11310741;
MAND X., Allen R., Ding X., Goellner M., Maier T., de Boer J.M.,
Baum T.J., Hussey R.S., Davis E.L.;
"Signal peptide-selection of cDNA cloned directly from the esophageal
gland cells of the soybean cyst nematode Heterodera glycines.";
Mol. Plant Microbe Interact. 14:536-544(2001).
-- SIMILARITY: Belongs to the SELT family.
                                                                                                                                                                                                                                                                                                                                                                      18 EPGSGVRIVVEYCEPCGF--EATYL--ELASAVKEQYPGIE-IESRLGGTGAFEIEINGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Putative esophageal gland cell secretory
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                            Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T., Hammon N., Israni S., Pitluck S., Richardson P.; Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heterodera glycines (Soybean cyst nematode worm).
Eukaryota, Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                  ; Score 116.5; DB 2; Length 104;
; Pred. No. 0.0019;
16; Mismatches 35; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative esophageal gland cell secretory protein 6 precursor
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                         GO; GO:0008430; F:selenium binding; IEA.
GO; GO:004545; P:cell redox homeostasis; IEA.
InterPro; IPR011893; CXXU selWTH.
InterPro; IPR071893; Selenow rel.
Pfam; PF05169; Selenow xel; I.
TIGREAMS; TIGR02174; CXXU selWTH; 1.
SEQUENCE IO4 AA; 11690 WW; AB6A6793EEDB4ACI CRC64;
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/FTId=PRO 0000032296.
Redox-active (Potential).
; DD94A7A590AA9143 CRC64;
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InterPro; IPR011193; CXXU selWTH.
ITGRPAMS; TIGR02174; CXXU_selWTH, 1.
Hypothetical protein; Redox-active center; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-NOV-2001, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                             EMBL; AAFG02000004; EAN56920.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 AA
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                                                    US DOE Joint Genome Institute (JGI-PGF);
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27201 MW;
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Best Local Similarity 34.11
Matches 30; Conservative
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                                                                                                                                 preliminary data.
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NECECTION SEQUENCE LLARGE SCALE WRONG).

TISSUB-Brain, PNS, Testing and Uterus;

MEDLINE=22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feirgold B.A., Grouse L.H., Derge J.G.,

A Rlausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Haieh F.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Haieh F.,

B Dronsfein M.J., Uddin T.B., Toshiyuki S., Carninoi P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Roas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

R Richards S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shorchenko Y., Boutfard G.G.,

R Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

B Lakesley R.W. Touchman J.W., Green E.D., Dickson M.C.,

Rutherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Roherchial Y.S.N., Krzywinski M.I., Marra M.A.,

R Generation and initial analysis of more than 15,000 full-length human
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
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MEDLINE=97398151; PubMed=9256076; DOI=10.1016/S0378-1119(97)00113-3;
Whanger P. P., Bellstein M.A., Vendeland S.C., Lugade A., Ream W.,
Whanger P.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Conserved features of selenocysteine insertion sequence (SECIS) elements in selenoprotein W cDNAs from five species."; Gene 193:187-196(1997).
                                                                                           . 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 --IESRLGGTGAFEIEINGQLVFSKLENGGFPYEKDLIE-----AIRRASNG
19.2%; Score 114.5; DB 1; Length 244; 22.5%; Pred. No. 0.008; ive 15; Mismatches 30; Indels 89.
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"Genomic structure of human selenoprotein W (SEPW1).";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bellingham J., Gregory-Evans C.Y.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEPW1 HUMAN STANDARD; PRT; 86 AA. P63302; 015532; 019096; Q86T19; Q96KM5; 11-0CT-2004, integrated into UniProtKB/Swiss-Prot. 11-0CT-2004, sequence version 1.
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Search completed: December 6, 2006, 10:39:47 Job time : 151 secs

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/EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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                  GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd
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US-09-393-448-3
US-09-393-448-3
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US-09-393-448-1
US-09-393-448-1
US-09-252-991A-17867
US-09-252-991A-17867
US-09-248-796A-17066
US-09-248-796A-17066
US-09-252-991A-22821
US-09-152-74-6
US-09-252-991A-29381
US-10-163-214-13
US-09-433-241A-10
US-09-433-241A-10
US-09-433-241A-10
US-09-433-241A-10
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| Sequence 7234, Application US/09513999C
| Patent No. 6783961
| APPLICANT: Dumas Milline Edwards, J.B.
| APPLICANT: Duclert, A.
| APPLICANT: Duclert, A.
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
| Patent No. 6783961
| CURRENT APPLICATION NUMBER: US/09/513,999C
| CURRENT PILLING DATE: 1990-02-24
| PRIOR FILING DATE: 1999-02-26
| NUMBER OF SEQ ID NOS: 36681
| SOFTWARE: Patent.pm
| SEQ ID NO 7234
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Sequence
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Pred. No. 4.5e-40;
2; Mismatches 9; Indels
                                                US-09-473-185A-699
US-09-907-175A-339
US-09-907-175A-339
US-09-905-775A-339
US-09-906-700-339
US-09-906-648-339
US-09-906-648-339
US-09-906-648-339
US-09-906-648-339
US-09-906-648-339
US-09-906-738-339
US-09-906-738-339
US-09-906-738-339
US-09-906-738-339
US-09-906-738-339
US-09-906-738-339
US-09-906-738-339
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US-09-906-738-339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIGAFEIEINGOLGVLQXGEWGFPYEKDV 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
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COTHER INFORMATION: Xaa=Asp or Glu
FRATURE:
FRATURE:
LOCATION: 46
OTHER INFORMATION: Xaa=Leu or Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 78
OTHER INFORMATION: Xaa=Ala or Gly
-09-513-999C-7234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 87.6%;
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
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COUNTRY SA104
COMPITER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
                                                                                                                                                                           SOFTWARE: FABLSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: GenBank
CLONE: 993035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-127-289-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 VRIVVEYCEPCGFEATYLELASAVKEQYPG-IEI--ESRLGGTGAFEIEINGQLVFSKLE 79
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Sequence 3, Application US/08807043
; Sequence 3, Application US/08807043
; Patent No. 5856131
; GENERAL INFORMATION:
APPLICANT: Hiillman, Jennifer L. APPLICANT: Hiillman, Jennifer L. APPLICANT: GOli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN SELENOPROTEIN NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaccuticals, Inc. STREET: 3174 Porter Drive
CITY: Palo Alto
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Patent No. 5998371
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN SELENOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE Incyte Pharmaceuticals, Inc.
STREET: 31'4 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF-0202 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: Hereath
CLASSIFTCATION 1530
PRIOR APPLICATION 530
PRIOR APPLICATION BATA:
APPLICATION NUMBER:
FILING DATE: NORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
RERERENCE/DOCKET NUMBER: PF-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                              ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: GenBank
CLONE: 993035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                             US-08-807-043-3
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23 VRIVVEYCEPCGFEATYLELASAVKEQYPG-IEI--ESRLGGTGAFEIEINGQLVFSKLE 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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COMPUTER READABLE FORM:
MEDIUM TYPEs Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRRESEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hiillman, Jennifer L.
Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN SELENOPROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
16.2%; Score 96.5; DB 1;
Best Local Similarity 34.1%; Pred. No. 0.00096;
Matches 28; Conservative 17; Mismatches 26;
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/393,448
FILING DATE: 10-Sep-1999
FLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,043
                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION UNBER:
APPLICATION WINBER:
FILING DATE:
ATTONEY, AGENT INPORMATION:
NAME: Billings, Lucy J.
REGISTRATION WUMBER: 36,749
REPERENCE/DOCKET WUMBER: PF-0202 US
TELECOMMUNICATION INPORMATION:
TELEFONEY: 415-855-0555
                                                                                US/09/127,289
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Patent No. 6545129
GENERAL INFORMATION:
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23 VRIVVEYCEPCGFEATYLELASAVKEQYPG-IEI--ESRLGGTGAFEIEINGQLVFSKLE 79
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                                                                                                                                                                                                                                      Length 93;
                                                                                                                                                                                                                                   16.2%; Score 96.5; DB 1; 32.8%; Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hiillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN SELENOPROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SUFTWARE: FastSBO for Windows Version 2.0
SUFRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,289
                                                                                                                                                                                                                                                                                           18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Incyte Pharmaceuticals, Inc.
3174 Porter Drive
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bilings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0202
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09127289
Patent No. 5998371
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IBM Compatible
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 32.8%
Matches 21; Conservative
; TYPE: amino acid
; STRANDEDNES: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIERRAY: BLADNOT03
; CLONE: 1599862
US-08-807-043-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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LIBRARY: BLADNOT03
CLONE: 1599862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 NGGF 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 GDGY 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 VRIVVEYCEPCGFEATYLELASAVKEQYPG-IEI--ESRLGGTGAFEIEINGQLVFSKLE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.2%; Score 96.5; DB 2; Length 88; 34.1%; Pred. No. 0.00096; Live 17; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08807043

Patent No. 5856131
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL HUMAN SELENOPROTEIN
WIMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZDENSING STATE TO STATE 
                                                                                                                       PF-0202 US
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0202 US
TELECOMMUNICATION INFORMATION:
TRIEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE: 993035
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                       63 GDGYVDTESKFRK-LVTAIKAA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 NGGF-----PYEKDLIEAIRRA 96
                                 ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 28; Сопяртиз
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US-08-807-043-1
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ORGANISM:
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11 VRVV--YCGAXGYKSKYLQLKKKLEDEPPGRLDICGEGTSQAXGFFEVMVAGKLIHSKXK 68
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Pred. No. 0.001;
...-erches 20; Indels
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO for Windows Version 2.0
                                                                                                                                                                                   Sequence 1, Application US/09393448
Patent No. 6545129
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN SELENOPROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/393,448
FILING DATE: 10-5ep-199
CLASSIFICATION: CURROWN-
PRIOR APPLICATION BOTA:
APPLICATION NUMBER: 08/807,043
FILING DATE: CURROWN-
ATTORNEY/AGENT INFORMATION:
NAME: B111ngs, Lucy NEGISTRATION NUMBER: 36/79
REGISTRATION NUMBER: 36/79
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Mismatches
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US-09-270-767-46297
; Sequence 46297, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                          STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
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STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 32.8%;
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FELEX: <Unknown>
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                                                       80 NGGF 83
                                                                                            69 GDGY 72
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US-09-393-448-1
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GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVERTION: NUCLEIC ACID AND ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVERTION: ABROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196,136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER: US 60/094,190

PRIOR FILING DATE: 1999-07-27

NUMBER: PSEQ ID NOS: 33142

SEQ ID NO 17867
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Sequence 10006, Application US/09489039A

Patent No. 6610836

APPLICANT: GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
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APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILLE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46297
LENGTH: 216
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14.6%; Score 87; DB 2; Length 216;
Best Local Similarity 18.8%; Pred. No. 0.047;
Matches 25; Conservative 15; Mismatches 25; Indels
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ORGANISM: Drosophila melanogaster
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186 GRFPSPEVLFQII 198
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Matches 25; Conserv
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR PELICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                         297 PATASPAAPPAPSEPAAAPVVAGEGOGV-VKVOFVADCWTQVTDANGKVLVSALKRKGDS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 PGQTSVAPPPEEVEP----GSGVRIVVEYCEPCGFEATYLE---LASAVKEQYPG 52
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                                                                                                                                                                                                                                                                                                          19; Gaps
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                                                                                                                                                                                                                                                                                                       Indels
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APPLICANT: Allen, Stephen M.
APPLICANT: Broglie, Karlene H.
APPLICANT: Brutler, Karlene H.
APPLICANT: Thorpe, Catherine J.
ITLE OF INVENTION: Startch Synthase Isoform V
FILE REFERENCE: BB1520 US NA
CURRENT APPLICATION NUMBER: US/10/163,214
CURRENT APPLICATION NUMBER: 60/297,099
PRIOR FILING DATE: 2001-06-08
                                                                                                                                                                                                                                                     ; Score 71.5; Di
; Pred. No. 7.8;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
11.7%; Score 70; DB
Best Local Similarity 22.2%; Pred. No. 26;
Matches 18; Conservative 20; Mismatches
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                          60/094,190
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; Sequence 14338, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al
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; Sequence 13, Application US/10163214
; Patent No. 6849781
                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ), ORGANISM: Klebsiella pneumoniae
US-09-489-039A-14338
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22821
LENGTH: 400
                                                                                                                                                                                                                                                        Query Match 12.0%;
Best Local Similarity 29.5%;
Matches 26; Conservative 1
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SEQ ID NO 14338
LENGTH: 695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 22821, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         16 EVEPGSGVRIVVEYCEPCGF--EATYL--ELASAVKEQYPGIEIESRLGGTGAFEIEING
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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     PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 CGFEATYLELASAVKEQYPGIEIESRLGGTGAFEIEINGQLVFSKLE-NGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.1%; Score 72; DB 2; Length 352; 24.7%; Pred. No. 5.7; tive 14; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                               Query Match 13.9%; Score 83; DB 2; Length 119; Best Local Similarity 25.3%; Pred. No. 0.059; Matches 21; Conservative 17; Mismatches 39; Indels
                       FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
SEQ ID NO 10006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 LGAETFIDFTKEKDVVEAVKKATNG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-248-796A-17066
; Sequence 17066, Application US/09248796A
; Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 -----FPYEKDLIEAIRRASNG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :: ::|||| :| ::|
78 QQIWERKQDGGFFDAAELKRRVR 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 QLVFSKLENGGFPYEKDLIEAIR 94
                                                                                                                                                                                                                                7 TYPE: PRT
7 ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 24.7*
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Candida albicans
US-09-248-796A-17066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER:
     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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US-09-252-991A-22821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 17066
LENGTH: 352
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21 SGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLGGTGAFEIEINGQLVFSKLEN 80
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                                                                                                                                                                                                             12; Gaps
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                                                                                                                                                       Query Match
11.6%; Score 69; DB 2; Length 874;
Best Local Similarity 26.8%; Pred. No. 47;
Matches 22; Conservative 14; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
11.6%; Score 69; DB 2; Length 915;
Best Local Similarity 28.4%; Pred. No. 51;
Matches 23; Conservative 11; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-10-163-214-6

| Sequence 6, Application US/10163214
| Patent No. 6449781
| Patent No. 6449781
| APPLICANT: Allen, Stephen M.
| APPLICANT: Broglie, Karen E.
| APPLICANT: Butler, Karlene H.
| APPLICANT: Thorpe, Catherine J.
| APPLICANT: Thorpe, Catherine J.
| APPLICANT: Thorpe, Catherine J.
| APPLICANT: Butler, Karlene H.
| FILE REFERENCE: BB1520 US NA
| CURRENT APPLICATION NUMBER: G0/297,099
| PRIOR FILING DATE: 2001-06-08
| NUMBER OF SEQ ID NOS: 13
| SOFTWARKE: Microsoft Office 97
| LENGTH: 915
| TYPE: BRT
| ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                     807 -GETFLNADEKGINDALVRAIN 827
                                                                                                                                                                                                                                                                                                                                                                    81 GGFPY----EKDLIEAIRRASN 98
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) SEQ ID NO 13

) LENGTH: 874

) TYPE: PRT

) ORGANISM: Vigna unguiculata

US-10-163-214-13
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Db 850 GFTFVHPDEKALSCAMERAFN 870
Search completed: December 6, 2006, 10:40:50

Search completed: December 6, 2006, 10:40:50 Job time : 30 secs

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Page

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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                    Copyright
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- protein search, using sw model OM protein

6, 2006, 07:19:35 ; Search time 146 Seconds (without alignments) 360.136 Million cell updates/sec December Run on:

US-09-824-787B-2 597

score:

1 MSGEPGQTSVAPPPEEVEPG......ASNGETLEKITNSRPPCVIL 115 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2589679 segs, 457216429 residues Searched:

2589679 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

geneseqp1980s:*geneseqp2000s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2005s:* geneseqp2001s:* A_Geneseq_8:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:*

SUMMARIES

Description	Aag78997 Human C35	Aag77870 Human C35	Abp58560 Human sit	Abp43843 RIKEN 181	Adh13244 Human mal	Adk48916 Human bre	Adv60511 Human bre	Adx83703 Human C35	Aea15131 Human pol	Aea62447 Human C35	Aef13891 Human C35	Abp43055 Human ova	Aab43521 Human can	Adk49069 Human bre	Aea62539 Recombina	Abr47619 Breast ca	Adp84573 Human bre	Adp84574 Human bre	Aag03153 Human sec	Adk49067 Human bre	Adk50220 Human car	Adk50219 Human car	Adk50217 Human car
QI QI	AAG78997	AAG77870	ABP58560	ABP43843	ADH13244	ADK48916	ADV60511	ADX83703	AEA15131	AEA62447	AEF13891	ABP43055	AAB43521	ADK49069	AEA62539	ABR47619	ADP84573	ADP84574	AAG03153	ADK49067	ADK50220	ADK50219	ADK50217
% Query Match Length DB	115 4	115 4	115 5	115 5	115 8	115 8	115 9	115 9	115 9	115 9	115 10	124 5	131 3	131 8	149 9	206 6	207 8	208 8	90 3	8 06	75 8	65 8	65 8
% Query Match Le	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	78.1	78.1	67.5	67.5	48.9	48.7	48.6
Score	597	597	597	597	597	597	597	597	597	597	597	597	597	597	597	597	466.5	466.5	403	403	292	291	290
Result No.		~	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23

Adk50218 Human car	Adk50201 Human car	Adk50214 Human car	Adk50202 Human car	Adk50187 Human car	Adk50213 Human car	Adk50188 Human car	Adk50196 Human car	Adk50209 Human car	Adk50215 Human car	Adk50210 Human car	Adk50216 Human car	Adk50227 Human car	Adk50221 Human car	Adk50225 Human car	Adk50222 Human car	Adk50182 Human car	Adk50228 Human car	Adk50226 Human car	Adk50206 Human car	Adk50229 Human car	Adk50189 Human car
8 ADK50218	8 ADK50201	8 ADK50214	8 ADK50202	8 ADK50187	8 ADK50213	8 ADK50188	8 ADK50196	8 ADK50209	8 ADK50215	8 ADK50210	8 ADK50216	8 ADK50227	8 ADK50221	8 ADK50225	8 ADK50222	8 ADK50182	8 ADK50228	8 ADK50226	8 ADK50206	8 ADK50229	8 ADK50189
.6 75	.4 64	.4 73	8.4 73	.2 64	.2 64	8.2 73	.2 75	8.1 64		8.1 73		7.9 64	7.9 64	99 6.	7.9 73	7.9 73	7.9 73	.9	7.8 85	.7 64	.7 65
290 48	289 48	4	4	4	4	4	288 48	4	4	287 48	4	286 47	4	4	286 47	4	286 47	286 47	4	35 4	285 47
24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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AAG78997 standard; protein; 115 AA.
                   Human C35, a tumour antigen.
              (first entry)
              22-JAN-2002
         AAG78997;
RESULT 1
  AAG78997
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Human; C35; cytostatic; gene therapy; vaccine; tumour antigen; breast cancer; bladder cancer; tumour immunotherapy; chromosome 17q12.

Homo sapiens.

WO200174859-A2.

04-APR-2001; 2001WO-US010855. 11-OCT-2001

04-APR-2000; 2000US-0194463P

(UYRP) UNIV ROCHESTER

Borrello MA; Evans EE, Zauderer M,

N-PSDB; AAI71785, AAI71793. WPI; 2001-626383/72.

Novel C35 polypeptides and C35 genes useful in immunogenic compositions and vaccines, for inducing antibody and cell-mediated immunity against target cells, such as tumor cells that express C35 gene.

Claim 11; Fig 1; 331pp; English.

The present sequence is human C35. C35 is a novel tumour antigen that is overexpressed in human breast and bladder carcinoma. C35 is thought to be a promising candidate for tumour immunotherapy, in immunogenic compositions and vaccines, to induce antibody and cell-mediated immunity against target cells such as tumour cells that express C35 genes. The C35 gene aligns on human chromosome 17q12

Sequence 115 AA;

Query Match

100.0%; Score 597; DB 4; Length 115;

N

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Gaps

. 0

Indels

Length 115;

9 9

Matches

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61

AAG77870;

RESULT 2

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The invention relates to human site-specific recombinase motif-containing protein 12.63 (ABP58560) and nucleic acids encoding it (ABZ25755). The protein has a molecular weight of 12.63 kD. The invention also relates to a method for the recombinant production of the protein, an antagonist of the protein, and the use of the protein, gene and antagonist in therapeutic applications. Site-specific recombinase motif-containing protein 12.63 can be used in the treatment of a variety of diseases such as cancer and HIV (human immunodeficiency virus) infection. The present sequence represents human site-specific recombinase motif-containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSGEPGQTSVAPPPEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLG
                                                                                                                                                                                                                                                  1 MSGEPGQTSVAPPPEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLG
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                                                                                                                                                                                                                                                                                                                          61 GTGAFEIEINGQLVFSKLENGGFPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 115
                                                                                                                                                                                                                                                                                                                                                         61 GTGAFEIEINGOLVFSKLENGGFPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; site-specific recombinase motif-containing protein 12.63; recombinant production; gene therapy; cancer; tumour; HIV infection; human immunodeficiency virus; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptide-human protein 12.63 containing site-specific recombinase characteristic sequence fragment and polynucleotide for coding it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human site-specific recombinase motif-containing protein 12.63
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                                                                                                         100.0%; Score 597; DB 4;
100.0%; Pred. No. 1.3e-60;
ive 0; Mismatches 0;
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100.0%; Pred. No. 1.3e-60;
ive 0; Mismatches 0;
     promote an immune response against a cancerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 27 (Disclosure); 33pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BODE-) BODE GENE DEV CO LTD SHANGHAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP58560 standard; protein; 115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JAN-2001; 2001CN-00105072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JAN-2001; 2001CN-00105072
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Best Local Similarity 100.
Matches 115; Conservative
                                                                                                                                     Best Local Similarity 100.
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-742038/81.
N-PSDB; ABZ25755.
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                                                          Sequence 115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein 12.63
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                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP58560
     SXS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises a compound which contains one or more major
histocompatibility complex (MHC)-peptide complexes, and an antibody
geoficitio for a call surface marker. The complexes comprise an MHC class I
alpha chain, a beta-2 microglobulin molecule and an antigenic peptide
bound in the MHC groove. Alternatively, the complexes may comprise an MHC
class II alpha chain, an MHC class II beta chain, and an antigenic
peptide bound in the MHC groove. The complexes are linked to the carboxyl
terminus of the antibody. The compounds of the invention can be used as a
vaccine to modulate an immune response. The compounds of the invention

vaccine to modulate an immune response. The compounds of the invention

parsaitic infections; hyperproliferative disorders (e.g. neoplasms and
hypergammaglobulinaemia); viral infections (e.g. Hashimoto's disease,

crowse' disease and rheumatoid arthritis); allergic reactions/conditions

(e.g. asthma). The compounds of the invention may also be used in the
present sequence represents C35 protein, this protein is differentially

expressed in human breast cancer calls. In one embodiment of the
invention, antigenic peptides derived from the C35 protein can be used to
                                 ö
                                                                                      9
                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C35 protein; antigenic peptide; major histocompatibility complex; MHC-peptide complex; MHC; human; MHC class I alpha chain; beta-2 microglobulin; MHC class II alpha chain; MHC class II beta chain; vaccine; immune response modulation; hyperproliferative disorder; neoplasm; hypergammaglobulinaemia; viral infection; hepatitis; maningitis; bacterial infection; tuberculosis; gingivitis; parasitic infection; autoimmune disease; Hashimoto's disease; Graves' disease; rheumatoid arthritis; allergy; asthma; organ rejection; graft-versus-host disease; GVHD; breast cancer.
                                                                                                                                     1 MSGEPGQTSVAPPPEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLG
                                                                                   1 MSGEPGQTSVAPPPEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLG
                                 Gaps
                                                                                                                                                                                                                      GTGAFEIEINGQLVFSKLENGGFPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 115
                                                                                                                                                                                          61 GTGAFEIEINGQLVFSKLENGGFPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel compound comprising major histocmpatibility complex-peptide complexes, used to modulate immune responses.
                                 ö
                                 Indels
                                 ö
  Pred. No. 1.3e-60;
                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                               AAG77870 standard; protein; 115 AA
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100.001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-2002 (first entry)
                                 115, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zauderer M, Smith ES;
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  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human C35 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                    61 GTGAFEIEINGQLVFSKLENGGFPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 115
GTGAFEIEINGQLVFSKLENGGFPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 115
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100.0%; Pred. No. 1.3e-60;
iive 0; Mismatches 0;
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Yang Y, Wehrman T, Drmanac RT;
                                                                                                                                                                                                                                         ABP43843 standard; protein; 115 AA
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Best Local Similarity 100.
Matches 115; Conservative
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This invention relates to a novel method for the prediction, diagnosis, or prognosis of malignant neoplasia by the detection of at least two markers. The invention may also be useful for the development of cytostatic compounds through the regulation of the expression of a gene or activity of a protein associated with malignant neoplasia. The method is useful for prediction, diagnosis or prognosis of malignant neoplasia cancer, ovarian cancer, gastric cancer, colon cancer, cesophageal cancer, wesenchymal cancer, bladder cancer or non-small cell ung cancer. The polynucleotides and polypeptides defined in the specification, antisense polynucleotides targeting either one of the polynucleotides or polypeptides, and compounds identified by the screening methods are useful for preventing or treating malignant neoplasia. The disease treated is preventing or treating malignant neoplasia. The disease treated is preventing constant cancer, in the present sequence is that of a human of a human cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Predicting, diagnosing or prognosing malignant neoplasia by detecting at least two markers, where the markers are genes from one or more chromosomal regions altered in malignant neoplasia,.
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                                                                                                                                                                                                                                                                         malignant neoplasia; cytostatic; breast cancer; ovarian cancer; gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer; bladder cancer; non-small cell lung cancer; human.
61 GTGAFEIEINGQLVFSKLENGGFPYEKDLIEAIRRASNGFTLEKITNSRPPCVIL 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preferably breast cancer. The present sequence is that of a human malignant neoplasia-related protein which may be used in the method
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                                                                                                                                                                                                                                      Human malignant neoplasia-related protein SeqID93.
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                                                                                                                      ADH13244 standard; protein; 115
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13-FEB-2003; 2003EP-00003112.
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel isolated polypeptide comprising or consisting of two or more C35 peptide epitopes. The polypeptide of the invention demonstrates cytostatic activity and may be useful for the formulation of an immunogenic composition, such as a vaccine, to induce antibodies and cell-mediated immunity against target cells such as tumour cells. Furthermore, the polypeptide and its analogues may be useful as prognostic markers for carcinoma, such as human breast or bladder carcinoma rate current sequence is that of human breast/bladder carcinoma related C35 protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
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                                                                                                                                    C35 epitope, cytostatic; vaccine; tumour; breast; bladder carcinoma;
human; C35.
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100.0%; Score 597; DB 8; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.3e-60;
Matches 115; Conservative 0; Mismatches 0; Indels
                                                                                                            Human breast/bladder carcinoma-related C35 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1, SEQ ID NO 2, 626pp; English.
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                             ADK48916 standard; protein; 115 AA.
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11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
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                                                                                   04-NOV-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                         (VACC-) VACCINEX INC. (UYRP ) UNIV ROCHESTER
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                                                         ADK48916;
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ID ADV
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RESULT 6
ADK48916
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This invention relates to a novel secreted human marker proteins (MKs)
and the encoding nucleic acid molecules thereof. Specifically, it refers
to a method for assessing whether a patient has breast cancer that has
metastasized or is likely to metastasize. The present invention describes
determining the level of expression of a marker protein in the patient
sample and comparing this to the level from a control subject having a
non-metastasized breast tumor or no breast tumor. Furthermore it provides
a screening method for assessing the suitability of one or more test
compounds at inhibiting breast cancer in a patient by inhibiting the
corpounds at inhibiting the clinical outcome of a breast cancer
it is useful for predicting the clinical outcome of a breast cancer
batient, for monitoring progression of the disease and for assessing the
compounds compositions derived thereof exhibit cytostatic
activities. This polypeptide is a human breast cancer staging marker
protein of the invention.
                                                                                                                                                                                                                                                                                                                                 Glatt K;
, Schlegel R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel marker protein, useful for assessing whether patient is afflicted with breast cancer, for assessing efficacy of therapy for inhibiting breast cancer, for assessing breast cell carcinogenic potential of test
                 breast tumor; cytostatic; diagnosis; prognosis; tumour marker; cancer.
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                                                                                                                                                                                                                                                                                                                                 Hoersch S, Anderson DL, Endege WO, Ford D, G
BO, Kamatkar S, Xu Y, Gannavarapu M, Zhao X,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human C35 antigenic protein, seqid:2.
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                                                                                                                                                                                                                           29-MAY-2003; 2003US-0474281P.
23-MAR-2004; 2004US-055557P.
                                                                                                                                                                                  26-MAY-2004; 2004WO-US016793
                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Best Local Similarity 100.
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-039718/04.
N-PSDB; ADV60510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 115 AA;
                                                                                                   WO2004106495-A2.
                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                     Gorbatcheva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAY-2005
                                                                                                                                                                                                                                                                                                                                   Mohahan JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             composition
                                                                                                                                           09-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                             Mertens M:
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New compounds comprising major histocompatibility complex Class I-peptide -antibody conjugates with modified beta2-microglobulin, useful for modulating immune responses or for treating or preventing e.g. cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a novel targeted vaccine delivery system comprising one or more peptide-major histocompatibility complex (MHC) (class I complexes linked through the beta2-microglobulin molecule to an antibody which is specific for a cell surface marker. The invention is useful for modulating an immune response and for preventing and treating cancer, infectious diseases, autoimmune diseases and allergies. The present sequence is human C35 antigenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosis; prognosis; cancer; breast tumor; ovary tumor; stomach tumor; colon tumor; esophagus tumor; bladder tumor; non-small-cell lung cancer; cytostatic; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSGEPGQTSVAPPPEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLG
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             major histocompatibility complex, cancer; cytostatic; neoplasm, infectious disease; antimicrobial; infection; autoimmune disease; immunosuppressive; immune disorder; allergy; antiallergic; C35 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lery Match 100.0%; Score 597; DB 9; Length 1:
st Local Similarity 100.0%; Pred. No. 1.3e-60;
tches 115; Conservative 0; Mismatches 0; Indels
 gene therapy; adoptive immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 2; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEA15131 standard; protein; 115
                                                                                                                                                                            09-JUL-2004; 2004US-00887230
                                                                                                                                                                                                         10-JUL-2003; 2003US-0485716P.
22-OCT-2003; 2003US-0513043P.
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                                                                                                                                                                                                                                                         (VACC-) VACCINEX INC
                                                                                                                                                                                                                                                                                                                     WPI; 2005-180769/19
                                                                                                                                                                                                                                                                                                                                        N-PSDB; ADX83702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 115 AA;
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                                                                                                            US2005042218-A1
chemotherapy;
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                                                                              Homo sapiens
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                                                                                                                                            24-FEB-2005.
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                                                                                                                                                                                                                                                                                         Zauderer M;
                                                                                                                                                                                                                                                                                                                                                                                                                          infections
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1 MSGEPGQTSVAPPPEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLG 60
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                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of predicting response to cancer treatment comprising detection of at least 2 markers, where the markers are genes and fragments or genomic nucleic acid sequences that are located on one chromosomal region, which is altered in malignant neoplasia. The invention also relates to a method for the prediction, diagnosis or prognosis of malignant neoplasia, methods for detecting deregulations in malignant neoplasia and breast cancer, a method of determining the phenotype of a cell or tissue, a method for identifying genomic regions which are altered on the chromosomal level and encode genes that are linked by function and are differentially expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                malignant neoplasia and breast cancer, methods of screening for agents which regulate the activity of a polypeptide or a polynucleotide and antibodies that specifically bind to a full length or partial polypeptide. The method is useful for predicting response to cancer treatment. The methods and compositions are useful for predicting, including breast cancer, overtian or treating malignant neoplasia including breast cancer, ovariant cancer, gastric cancer, colon cancer, esophageal cancer, ovariant cancer, bladder cancer or non-small-cellung cancer. This sequence represents a human polypeptide used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GTGAFEIEINGQLVFSKLENGGFPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GTGAFEIEINGQLVFSKLENGGPPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 115
                                                                                                                                                                                                            Predicting a response to cancer treatment by detecting at least 2 markers, which are genes or genomic nucleic acid sequences that are located on one chromosomal region, which is altered in malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C35 antigen, antigen; cell growth; cancer; cytostatic; apoptosis;
immunotherapy; hyperproliferation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 597; DB 9; Length 115; 100.0%; Pred. No. 1.3e-60;
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                                                                                                                                                                                                                                                                                                              Claim 8; SEQ ID NO 93; 464pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEA62447 standard; protein; 115 AA
15-OCT-2004; 2004WO-EP011599
                                      28-OCT-2003; 2003EP-00024565.
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Best Local Similarity 100.
Matches 115; Conservative
                                                                           (FARB ) BAYER HEALTHCARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  scope of the invention.
                                                                                                                                                     WPI; 2005-372393/38.
N-PSDB; AEA15108.
                                                                                                                  Munnes M;
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                                                                                                                                                                                                                                                                            neoplasia.
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                                                                                                                Wirtz R,
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Gaps

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Length 115;

colorectal tumor; prostate tumor; pancreas tumor; lung tumor;

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administering an apoptosis-inducing therapy to cancer cells, and administering an apoptosis-inducing therapy to cancer cells, and administering to the cells an antibody specific for an intracellular, cancer-associated protein, provided that the protein is not C35 antigen, where protein becomes exposed on the cell surface in cells undergoing apoptosis, where the antibody is conjugated to or complexed with a toxin. The non-C35 antigen protein is a prenjugated to or complexed with a toxin. The non-C35 antigen protein is a prenjugated to or complexed with a toxin. The non-C35 antigen protein is a prenjugated to or complexed with a toxin. The non-C35 antigen protein [35] the Virelon an antibody comprising the Virelon encoded by clone 1826, the Viregion encoded by ARA62495, an antibody comprising the URA62497, a chimeric antibody, or a humanized antibody, a polynucleotide, a host conding the antibody, a vector comprising the polynucleotide, a host coll comprising the antibody, a vector and a composition comprising the antibody and a carrier. The method is useful for Killing cancer cells in a mammal preferably human in need of cradication of smaller tumors and/or micrometastages, or in need of cradication of smaller for S35-associated cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chosen from breast cancer, ovarian cancer, bladder cancer, lung cancer, prostate cancer, pancreatic cancer, colon cancer, melanoma and other hyperproliferative disorders. The antibody is useful for detecting, disgnosing or monitoring C35-associated cancers. The antibody comprises a chimeric antibody comprising human immunoglobulin constant regions fused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the variable regions of mouse anti-35 antibodies (named 1F2, 1B3, MAb 165 and MAb 171). The present sequence represents the human C35 antigen.
                                                                                                                                                                                                                                                                                                                                  Killing cancer cells, by administering apoptosis-inducing therapy and administering antibody specific for intracellular, cancer-associated protein other than C35, or antibody specific for C35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to killing (M1) cancer cells, comprising
                                                                                                                                                                                                  Zauderer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 115;
                                                                                                                                                                                               Smith ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, SEQ ID NO 2, 255pp; English
                                                                                                                                                                                                  Sahasrabudhe DM,
06-DEC-2004; 2004WO-US040573
                                                       04-DEC-2003; 2003US-0526572P.
23-DEC-2003; 2003US-0531688P.
                                                                                                                                                                                                  Evans EE, Paris MJ,
                                                                                                                                           (VACC-) VACCINEX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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N-PSDB; AEA62446.
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                                                                                                         1 MSGEPGQTSVAPPPEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLG
                                       Gaps
                                                                                                                                                     61 GTGAFEIEINGQLVFSKLENGGPPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 115
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                                     0; Indels
100.0%; Score 597; DB 9;
100.0%; Pred. No. 1.3e-60;
ive 0; Mismatches 0;
                                     Matches 115, Conservative
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Tumor marker; diagnosis; antigen; cancer; cytostatic; breast tumor;
                  AEF13891 standard; protein; 115 AA.
                                                     (first entry)
                                                                       Human C35 protein.
                                                     09-MAR-2006
                                    AEF13891;
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The invention relates to matching a cancer condition in a patient with an immunotherapeutic agent or immunotherapeutic regimen comprising assaying tumor tissue of the patient for two or more expressed tumor-associated antigens (TuAs) in a preselected panel, to develop an antigen profile for the tumor. Also included is a method of confirming a cancer diagnosis. At least one of the TuAs is a cancer testis antigen, profile appropriate one of the TuAs is a cancer testis antigen, tissue-specific antigen, oncofetal antigen, differentiation antigen, growth factor receptor, adhesion factor, signal transduction product, or a microbial antigen. The preselected panel comprises two or more antigens selected from an SSX protein, SSX-2, SSX-4, a MAGE protein, or tyrosinase, and where the cancer condition is carcinoma selected from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            breast, colorectal, prostate, pancreatic, lung, ovarian, renal cell, or melanocyte. The methods are useful for matching a cancer condition in a patient with an immunotherapeutic agent or immunotherapeutic regimen and for confirming a cancer diagnosis, where the cancer condition is carcinoma selected from breast, colorectal, prostate, pancreatic, lung, ovarian, renal cell, or melanocyte. The present sequence is a human tumor associated antigen used in the method of the invention, chosen from the
                                                                                                                                                                                                                                                                                                                                                                                                                  Matching a cancer condition in a patient with an immunotherapeutic agent comprises assaying tumor tissue for at least two expressed tumor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSGEPGQTSVAPPPEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLG
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100.0%; Pred. No. 1.3e-60;
ive 0; Mismatches 0;
                ovary tumor; renal tumor; melanoma; immunotherapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human ovarian antigen HVCAA68, SEQ ID NO:4187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, SEQ ID NO 11; 104pp; English.
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                                                                                                                                                                           17-JUN-2005, 2005WO-US021836.
                                                                                                                                                                                                                  17-JUN-2004; 2004US-0580969P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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Matches 115; Conservative
                                                                                                                                                                                                                                                                                               Chiang C, Simard JJL;
                                                                                                                                                                                                                                                         (MANN-) MANNKIND CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated antigens.
                                                                                                                                                                                                                                                                                                                                      WPI; 2006-090202/09
                                                                                                                                                                                                                                                                                                                                                                             REFSEQ, NP_115715.
                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AEF13911
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                                                                                               WO2006002114-A2.
                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-2002
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Best Local 8
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ID ABP4
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AC ABP4
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DT 22-1
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N-PSDB; ABQ56132.

ovarian cancer, breast cancer; tumour; reproductive system disorder; noterility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; synaecological; reproductive. ovarian antigen; ovary; ovarian; breast; cancer; tumour;

Homo sapiens.

WO200200677-A1

03-JAN-2002.

07-JUN-2001; 2001WO-US018569

07-JUN-2000; 2000US-0209467P

(HUMA-) HUMAN GENOME SCI INC

Birse CE, Rosen CA;

WPI; 2002-147878/19

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.

Claim 11; SEQ ID NO 4187; 2922pp; English.

The invention relates to 2.17 mover numen ovarian antigens (ABP41224) and also encompasses polypeptides 90% identical and polynucleotides 95% identical compasses polypeptides 90% identical and polynucleotides 95% identical compasses polypeptides 90% identical and polynucleotides 95% identical compasses polypeptides 90% identical numen ovarian antigen polynucleotides and bost cells comprising human ovarian antigen polynucleotides and polypeptides in diagnossing, recombinant vectors and host cells and polypeptides in diagnossing, treating, prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and disorders (e.g., infertility, disorders of pregnancy, anovulation, oplycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HTV, toxoplaemosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and varior shock syndrome), inflammatory conditions (e.g., mastitis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and varior shock syndrome), inflammatory conditions (e.g., mastitis, systemic lupus erythematosus), conditions (e.g., mastitis, systemic lupus erythematosus), chood-related disorders (e.g., anaemia), cardiovascular disorders and urinary system disorders (e.g., anaemia), cardiovascular disorders and urinary system disorders (e.g., anaemia), cardiovascular disorders and urinary system disorders (c.g., anaemia), cardiovascular disorders (c.g., congoulate ovarian antigen expression or activity. The polynucleotides may also be used in screening for modulate ovarian antigen expression or activity. The polynucleotides may also see therapy, chromosome mapping, in the modulate ovarian antigen system of and ditives or to prepare antibodies cuseful in disease disaposis, drug targeting and phenotyping. The present esquence data for this patent dia net compounds which or sequence data for this patent dia network or to prepare antibodies or p invention relates to 2175 novel human ovarian antigens (ABP41054ftp.wipo.int/pub/published_pct_sequences

Sequence 124 AA;

ö ö Length 124; 0; Indels Query Match 100.0%; Score 597; DB 5; Best Local Similarity 100.0%; Pred. No. 1.5e-60; 0; Mismatches Matches 115; Conservative

69 10 MSGEPGGTSVAPPPEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLG 61 GTGAFEIEINGQLVFSKLENGGFPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 115 70 GTGAFEIEINGQLVFSKLENGGFPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 124 염

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RESULT 13 AAB43521

AAB43521 standard; protein; 131 AA

AAB43521;

08-FEB-2001 (first entry)

Human cancer associated protein sequence SEQ ID NO:966.

Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidhebetic; antisthratic; antistrematic; antiathritic; antiviral; antiinflammatory; antithyroid; antiallergic; antiacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ refection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.

Homo sapiens.

21-SEP-2000.

38-MAR-2000; 2000WO-US005882

99US-0124270P 12-MAR-1999; (HUMA-) HUMAN GENOME SCI INC

Rosen CA, Ruben SM;

WPI; 2000-587533/55. N-PSDB; AAC77730. Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.

Claim 11; Page 1534-1535; 2352pp; English.

AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB3338 to AAB4239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antialergic; antiarthritic; antinflammatory; antithyroid; antialergic; antibacterial; antiviral; cermationfogical, neuroprotective; cardiant; thrombolytic; coagulant; cootropic; vasotropic; antipacriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of isorders, allergic reactions, differentiation or mobilisation of cisorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate confinemantion, cancers, cardiovascular disorders, nucleotides, antibodies, bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in the exemplification of AAC78457 and AAB44240 represent sequences used in the exemplification of the present invention

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                                                                                                                                                                                                   9
                                                                                                                                                                                                                                        17 MSGEPGQTSVAPPPPEEVEPGSGVRIVVEYCEPCGFEATYLLELASAVKEQYPGIEIESRLG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel C35 polypeptide useful for formulation of immunogenic composition to induce antibodies and cell-mediated immunity against tumor cells.
                                                                                                                                                                                                   MSGEPGQTSVAPPPEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLG
                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                       GTGAFEIEINGQLVFSKLENGGFPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma;
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                                                             100.0%; Score 597; DB 3;
100.0%; Pred. No. 1.6e-60;
ive 0; Mismatches 0;
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11-DEC-2002; 2002US-0432241P.
23-APR-2003; 2003US-0464650P.
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                                                                                               Best Local Similarity 100. Matches 115, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-062349/06.
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Sequence 131 AA;
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The invention relates to killing (MI) cancer cells, comprising administering an apoptosis-inducing therapy to cancer cells, and administering to the cells an antibody specific for an intracellular, cancer-associated protein, provided that the protein is not C35 antigen, where protein becomes exposed on the cell surface in cells undergoing apoptosis, where the antibody is conjugated to or complexed with a toxin. The non-C35 antigen protein is a prenylated protein. Also included are an isolated antibody [1] specific for C35 (chosen from an antibody comprising the VH region encoded by clone 1836, the VL region encoded by clone 1826, the VL region encoded by clone 1828, the VH region encoded by clone 1826, the VL region encoded by clone 1828, the VH region encoded by clone 1826, the VL region encoded by ABA62495, an antibody comprising at least one of CDR1 or CDR2 of the VH region encoded by ABA62495, an antibody comprising at least one of CDR1, CDR2, or CDR3 of the VL region encoded by ABA62497, a chimeric antibody, or a humanized antibody, a polynucleotide concerned a composition comprising the antibody and a cardication of smaller tumors and of cancer call comprising the vector and a composition comprising the antibody and a cardication of smaller tumors and other concerning the antibody composition of smaller tumors and other chosen from breast cancer, ovarian cancer, bladder cancer, lung cancer, chosen from breast cancer, ovarian cancer, melanoma and other chosen from breast cancer, colon cancers melanoma and other chosen ground cancer, pancreatic cancer, colon cancers melanoma and other chosen from breast cancer, ovarian cancer, bladder cancer, lung cancer, chosen from breast cancer, colon cancers melanoma and other chyperproliferative disorders. The antibody cancer colon cancer calls in a m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Killing cancer cells, by administering apoptosis-inducing therapy and administering antibody specific for intracellular, cancer-associated protein other than C35, or antibody specific for C35.
GTGAFELEINGQLVFSKLENGGFPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 131
                                                                                                                                                                                                                                                                                                                       C35 antigen, antigen; cell growth; cancer; cytostatic; apoptosis;
immunotherapy; hyperproliferation; epitope mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "His-tagged signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "C35 antigen"
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                                                                                                                                         AEA62539 standard; protein; 149
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23-DEC-2003; 2003US-0531688P.
                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .149
                                                                                                                                                                                                                                                                            Recombinant C35 antigen.
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Synthetic.
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Gaps

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Matches 115; Conservative

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17 MSGEPGQTSVAPPPPEEVEPGSGVRIVVEYCEPCGPEATYLELASAVKEQYPGIEIESRLG 76

61 GTGAFEIEINGQLVFSKLENGGFPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 115

1 MSGEPGQTSVAPPPEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLG

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to the variable regions of mouse anti-35 antibodies (named 1F2, 1B3, MAb 165 and MAb 171). The present sequence represents a recombinant human C35 antigen (with a used His-tagged signal peptide), Lys-C digests of which were used in epitope mapping studies.
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Sequence 149 AA;

Gaps 0; Query Match
Best Local Similarity 100.0%; Pred. No. 1.9e-60;
Matches 115; Conservative 0; Mismatches 0; Indels (

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Search completed: December 6, 2006, 09:24:45 Job time : 149 secs

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LENGTH: 115
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Sequence 38691, A
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Sequence 10642, A
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/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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1 MSGEPGQTSVAPPPEEVEPG......ASNGETLEKITNSRPPCVIL 115
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd
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US-11-1053-818-86
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US-10-264-049-4187
US-09-925-301-966
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Maximum Match 100%
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Sequence 93, Application US/10435696
Publication No. US20040018525A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wintz, Ralph
APPLICANT: Winnes, Marc
APPLICANT: Kallabis, Harald
APPLICANT: Kallabis, Harald
TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
FILE REFERENCE: LeA 36 108
CURRENT APPLICATION NUMBER: US/10/435,696
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: EP03003112.4
                                                      Sequence 12886, A Sequence 12813, A Sequence 12113, A Sequence 10109, A Sequence 10108, A Sequence 13121, A Sequence 31232, A Sequence 163110, Sequence 163110, Sequence 163110, Sequence 163110, Sequence 163110, Sequence 163110,
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| GENERAL INFORMATION:
| APPLICANT: Zauderer, Maurice
| APPLICANT: Zauderer, Maurice
| APPLICANT: Evans, Elizabeth E.
| APPLICANT: Borrello, Melinda A.
| TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
| TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
| FILE REFERENCE: 1821.0040001
| CURRENT APPLICATION NUMBER: US/09/824,787B
| CURRENT FILING DATE: 2001-04-04
| PRIOR FILING DATE: 2000-04-04
| NUMBER OF SEQ ID NOS: 1471
| SOFTWARE: Patentin Ver. 2.1
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100.0%; Score 597; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.3e-58;
Matches 115; Conservative 0; Mismatches 0; Indels
                                         US-10-614-853-14
US-10-614-853-14
US-10-369-493-122836
US-10-369-493-12313
US-11-096-568A-10110
US-11-096-568A-10109
US-11-096-568A-10108
US-11-096-568A-31233
US-11-096-568A-31233
US-11-096-568A-31233
US-11-096-568A-31233
US-11-096-568A-31233
US-11-036-368A-31233
                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
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ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: human
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                                                                                                           LENGTH: 115
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Publication No. US20050042218A1
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: MHC Class I - Peptide-Antibody Conjugates with Modified
TITLE OF INVENTION: B2-Microglobulin
FILE REFERENCE: 1843.0160002
CURRENT PILIGNED DATE: 2004-07-09
PRIOR APPLICATION NUMBER: US 60/485,716
PRIOR FILING DATE: 2003-7-10
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APPLICANT: Evans, Elizabeth E.
APPLICANT: Evans, Elizabeth E.
APPLICANT: Borrello, Melinda A.
TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
FILE REPERENCE: 1821.0040005
CURRENT FILING DATE: 2003-06-10
PRIOR APPLICATION NUMBER: US 60/464,650
PRIOR APPLICATION NUMBER: US 60/464,650
PRIOR SEC ID NOS: 160
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2.
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100.0%; Pred. No. 2.3e-58;
cive 0; Mismatches 0;
PRIOR FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: EP02010291.9
PRIOR FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 314
SOFTWARE: Patentin version 3.1
SEROID NO 93
LENGTH: 115
TYPE: PRI
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Best Local Similarity 100.
Matches 115; Conservative
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                                                                                                                                                                          ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-457-829-2
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US-10-80-30-80-80

Sequence 86, Application US/1085588

Publication No. US20050042642A1

GENERAL INFORMATION:

APPLICANT: Mondan, John

APPLICANT: Mondrano, Dustin

APPLICANT: Enderson, Dustin

APPLICANT: Enderson, Dustin

APPLICANT: Gorbatcheva, Bella

APPLICANT: Gorbatcheva, Bella

APPLICANT: Gorbatcheva, Manjula

APPLICANT: Granavarapu, Manjula

APPLICANT: Zhao, Xumei

APPLICANT: Cannavarapu, Manjula

APPLICANT: Mureen Mertens

TITLE OF INVENTION: IDENTIFICATION, XSSESSMENT, PREVENTION, AND THERAPY OF

TITLE OF INVENTION: IDENTIFICATION

TITLE OF INVENTION: UNBER: 60/474,281

FRIOR APPLICATION NUMBER: 60/474,281

FRIOR APPLICATION NUMBER: 60/555,557

FRIOR APPLICATION NUMBER: 60/555,557

FRIOR APPLICATION NUMBER: 60/555,557

FRIOR APPLICANTION NUMBER: 60/555,557

FRIOR APPLICANTION NUMBER: 60/555,557

FRIOR APPLICANTION NUMBER: 60/555,557

FRIOR ENTING DATE: 2000-05-29

SEQUID NO 86

SOFTWARE: FRANCE FRIENCE

TITLE OF INVENTION: 100-05-29

SOFTWARE: PRESENCE FRIENCE

SOFTWARE: PRESENCE

TITLE OF INVENTION: 100-05-29

SOFTWARE: PRESENCE

SOFTWARE: PRESENCE

TITLE OF INVENTION: 100-05-29

SOFTWARE: PRESENCE

TITLE OF INVENTION: 100-05-29
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100.0%; Pred. No. 2.3e-58;
tive 0; Mismatches 0;
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100.0%; Pred. No. 2.3e-58;
iive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 60/513,043 PRIOR FILING DATE: 2003-10-22 NUMBER OF SEQ ID NOS: 55 SOFTWARE: Patentin version 3.2 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 115; Conservative
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Best Local Similarity 100.0
Matches 115; Conservative
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1 MSGEPGQTSVAPPPEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLG 60
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      US-11-233-510-6

Sequence 6, Application US/11233510

Sequence 6, Application Wo. US2006063190A1

GENERAL INFORMATION:

APPLICANT: Fischer, Timchy J.

APPLICANT: Malinowski, Douglas P.

APPLICANT: Marcalpoil, Raphael

APPLICANT: Morel, Didier

TITLE OF INVENTION: Methods and Compositions for Evaluating

TITLE OF INVENTION: Breast Cancer Prognosis

TITLE OF INVENTION: Breast Cancer Prognosis

TITLE OF INVENTION: Methods and Compositions for Evaluating

TITLE OF INVENTION: Morel, Didier

TITLE OF INVENTION: Breast Cancer Prognosis

TITLE OF INVENTION: Breast Cancer Prognosis

TITLE OF INVENTION: Breast Cancer Prognosis

FILE REFERENCE: 46143/296318

CURRENT FILING DATE: 2004-09-22

FRIOR FILING DATE: 2004-09-22

NUMBER OF SEQ ID NOS: 41

SOPTWARE: FASTESEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 115

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100.0%; Score 597; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-58;
Matches 115; Conservative 0; Mismatches 0; Indels 0
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; Sequence 34, Application US/09833203
; Publication No. US20030166277A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice
APPLICANT: Smith, Ernest S.
; TITLE OF INVENTION: Targeted Vaccine Delivery Systems
; FILE REFERENCE: 1821.0020001
; CURRENT APPLICATION NUMBER: US/09/833,203
; CURRENT FILING DATE: 2001-04-12
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 34
; LENGTH: 117
; TYPE: PRI
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OTHER INFORMATION: C35
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Sequence 2, Application US/11003819
; Publication No. US20050158323A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Faris, Mark J.
; APPLICANT: Sahasrabudhe, Deepak M.
APPLICANT: Sahasrabudhe, Deepak M.
APPLICANT: Sahasrabudhe, Deepak M.
APPLICANT: Sahasrabudhe, Deepak M.
TITLE OF INVENTION: Methods of Killing Tumor Cells by Targeting Internal Antigens
TITLE OF INVENTION: Methods of Killing Tumor Cells
FILE REPERENCE: 1843 0190002
CURRENT APPLICATION NUMBER: US/11/003,819
CURRENT APPLICATION NUMBER: US 60/256,572
FRIOR APPLICATION NUMBER: US 60/256,572
FRIOR APPLICATION NUMBER: US 60/531,688
FRIOR FILING DATE: 2003-12-04
FRIOR APPLICATION NUMBER: US 60/531,688
; PRIOR APPLICATION UMBER: US 60/531,688
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Publication No. US20060008468A1
Sequence 11, Application No. US2006000846BA1
GENERAL INFORMATION:
APPLICANT: Chiang, Chih-Sheng
APPLICANT: Simard, John J.L.
TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
TITLE OF INVENTION: ANTIGENS IN DIAGNOSTICS FOR VARIOUS TYPES OF CANCERS
FILE REFERENCE: MANNK.050A
CURRENT FILING DATE: 2005-06-17
PRIOR PILING DATE: 2004-06-17
PRIOR FILING DATE: 2004-06-17
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
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Best Local Similarity 100.0
Matches 115; Conservative
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US-11-155-288-11
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RESULT 13
US-10-177-293-480
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APPLICANT:
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GTGAFEIEINGQLVFSKLENGGFPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 115
                        63 GTGAFEIEINGGLVFSKLENGGFPYEKDLIEAIRRASNGETLEKITNSRPPCVIL 117
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                                                                                                                                      Sequence 4187, Application US/10264049

| Publication No. US2004000557941
| CENERAL INFORMATION:
| APPLICANT: Bitse et al.;
| TITLE OP INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA133P1
| CURRENT FILING DATE: 2002-10-04
| PRIOR PILING DATE: 2001-06-07
| PRIOR PILING DATE: 3001-06-07
| PRIOR FILING DATE: 3001-06-07
| PRIOR FILING DATE: 3001-06-07
| PRIOR FILING DATE: 311
| SEQ ID NO 4187
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Patent No. US200205230841

GENERAL INFORMATION:

APPLICANT: ROBER et al.

TITLE OF INVENTION:

FILE REFERENCE: PA106

CURRENT FALLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR PILING DATE: 2000-03-08

PRIOR PILING DATE: 2000-03-08

PRIOR PILING DATE: 1999-03-12

NUMBER OF SEC ID NOS: 1694

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 966
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100.0%; Pred. No. 2.7e-58;
tive 0; Mismatches 0; Indels (
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Best Local Similarity 100.
Matches 115; Conservative
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Matches 115; Conservative
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US-09-925-301-966
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; ORGANISM: Homo sapiens
US-10-264-049-4187
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US-09-925-301-966
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APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Pusztai, Lajos
APPLICANT: Pusztai, Lajos
APPLICANT: Matic, Funda
APPLICANT: Mails, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS POR IDENTIFICATION, ASSESSMENT, FILLS OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILL REFERENCE: MRI-038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSGEPGQTSVAPPPEEVEPGSGVRIVVEYCEPCGFEATYLELASAVKEQYPGIEIESRLG
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Sequence 155, Application US/10457829
| Sequence 155, Application US/10457829
| Publication No. US2004006397A1
| GENERAL INFORMATION:
| APPLICANT: Zauderer, Maurice
| APPLICANT: Evans, Elizabeth E. |
| APPLICANT: Evans, Elizabeth E. |
| APPLICANT: Borrello, Mellinda A. |
| TITLE OF INVENTION: A Gene Differentially Expressed in Breast and TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides TITLE OF INVENTION WIMBER: US/10/457,829
| CURRENT APPLICATION NUMBER: US/0464,650 |
| PRIOR APPLICATION NUMBER: US 60/464,650 |
| PRIOR PILING DATE: 2003-06-10 |
| NUMBER OF SEQ ID NOS: 160 |
| SOFTWARE: PatentIn Ver. 2.1 |
| SEQ ID NO 155 |
| LENGTH: 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 597; DB 4; Length 131; Best Local Similarity 100.0%; Pred. No. 2.7e-58; Matches 115; Conservative 0; Mismatches 0; Indels (
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PRIOR APPLICATION UNDER: US 60/299,887
PRIOR PILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR PLING DATE: 2001-06-27
PRIOR PLING DATE: 2001-07-18
PRIOR PILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
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Publication No. US20030124128A1
GENERAL INFORMATION:
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APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumen
APPLICANT: Gannavarpu, Manjula
APPLICANT: Gannavarpu, Manjula
APPLICANT: Kamatkar, Shubhangi
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Wang, Youzhen
Xu, Yongyao
Hoersch, Sebastian
Monahan, John
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CORGANISM: Homo sapiens
US-10-457-829-155
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Search completed: December 6, 2006, 10:50:07 Job time : 85 secs
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; Sequence 153, Application US/10457829
; Publication No. US20040063907A1
; GREERAL INFORMATION:
GAPPLICANT: Zauderer, Maurice
; APPLICANT: Evans, Elizabeth E.
APPLICANT: Borrello, Melinda A.
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
; TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast
; TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
; TITLE OF INVENTION NUMBER: US/10/457,829
; CURRENT FILING DATE: 2003-06-10
; PRIOR FILING DATE: 2003-06-10
; PRIOR FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 153
; LENGTH: 90
; TYPE: PRT
 ORGANISM: Homo sapiens
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Pred. No. 7.3e-37;
2; Mismatches 9; Indels
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NAME/KEY: MISC_FEATURE
LOCATION: (46)...(46)
OTHER INFORMATION: Xaa is an unknown amino acid
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OTHER INFORMATION: Xaa is an unknown amino acid
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PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/XXX,XXX
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOGTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 480
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Best Local Similarity 87.6%;
Matches 78; Conservative
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                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Homo sapiens
US-10-177-293-480
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US-10-457-829-153
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: CLOOO728
GURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.9%; Score 148.5; DB 6; 34.0%; Pred. No. 2e-08; live 17; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 FPYEKDLIEAIRRASNGETLEKITNSR-PPCVIL 115
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PRIOR APPLICATION NUMBER: 60/157,832

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR PILING DATE: 1999-10-05

PRIOR PILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-28

PRIOR FILING DATE: 2000-01-2

PRIOR FILING DATE: 2000-01-2

PRIOR FILING DATE: 2000-01-2

PRIOR PILING DATE: 2000-01-2

PRIOR PILING DATE: 2000-01-2

PRIOR FILING DATE: 2000-03-24

PRIOR FILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SEQ ID NO 38691

LENGTH: 95
Sequence 38691, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 34.0%
Matches 32; Conservative
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